

File: 014_286_1810
Email: mousset@watson.wustl.edu
This clone is available regularly (see thread list, contact the
IMAGE Consortium (info: image@iml.uov) for further information.
MGI:284413

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.

FEATURES:

SOURCE:

Location/Qualifiers
1..37

/organism "Mus musculus"

/db_xref "taxon:10090"

/clone_db "MGI:284413"

/clone_db "MGI:284413"

/db_xref "GeneID:10990"

/db_xref "GeneID:10990"

/note "Vector: pTZ19 (ampicillin resistant)"

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/db_xref "GeneID:10990"
/note "Vector: pTZ19 (ampicillin resistant)"
This clone is available regularly (see thread list, contact the
IMAGE Consortium (info: image@iml.uov) for further information.
MGI:284413

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Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.

FEATURES:

SOURCE:

Location/Qualifiers
1..37

/organism "Mus musculus"

/db_xref "taxon:10090"

/clone_db "MGI:284413"

/clone_db "MGI:284413"

/db_xref "GeneID:10990"

/db_xref "GeneID:10990"

/note "Vector: pTZ19 (ampicillin resistant)"

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/note "Vector: pTZ19 (ampicillin resistant)"

/note "Vector: pTZ19 (ampicillin resistant)"

/note "Vector: pTZ19 (ampicillin resistant)"

REFERENCE

AUTHORS

Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha: Ephyridiidae: Ephyridiinae: Protophila
 1 (bases 1 to 40)
 Liao, G.-C., Rehm, E.J. and Rubin, G.M.
 Insertion site preferences of the P transposable element in *Drosophila melanogaster*
 Proc. Natl. Acad. Sci. U.S.A. 97 (7): 3347-3351 (2000)

JOURNAL

COMMENT

Contract: Gerald Rubin
 Berkeley Drosophila Genome Project
 University of California, Berkeley
 USA Building, Berkeley, CA 94720-3200, USA
 Fax: 5106439947
 Email: gerry@cellbio.berkeley.edu

Sequence recovery method was inverse PCR
 Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 001 in the 40 bases. This insertion position refers to the first base of the 9 base target recognition sequence.
 Class: transposon-tagged
 Location/Qualifiers

FEATURES

source

1..40
 Location/Qualifiers

/organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="Drosophila melanogaster EP line"
 /note="Inverse PCR was performed on *Drosophila* melanogaster strains each of which contains a single EP transposable element insertion. (The denaturation of these insertion strains is described in Reith P, Szabo K, Bailey A, Laverly T, Rehm J, Rubin GM, Weigmann R, Milau M, Benes V, Ansoy W, Cohen SM, 1998, Systematic gain-of-function genetics in *Drosophila*. Development 6, 1043-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <http://fruitfly.berkeley.edu/EP-Insertion/Inverse-PCR.html>."

BASE COUNT

7 a 13 c 12 g 8 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pled. No. 9e-04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUERY

8 CGTTGAGCAT 17
 |||||

DB

35 CGTTGAGCAT 26

RESULT 10

BH639055

LOCUS

DEFINITION

BH639055 1298627/AT111E11 1008 - *Drosophila* Grid 1 79a may's genome, DNA

ACCESSION

BH639055

VERSION

BH639055.1 GI:11000412

KEYWORDS

GSS.

SOURCE

ORGANISM

29a may's.
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Focales, Foucaceae, PACC clade, Pautioideae, Audoubernieae, Zea.
 1 (bases 1 to 40)
 Walbot, V.
 Maize genome sequences found using engineered RescueMu transposon
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genome sequences found using engineered RescueMu transposon
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA

FEATURES

source

1..40
 Location/Qualifiers

BASE COUNT

12 a 5 c 14 g 9 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pled. No. 9e-04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUERY

27 TGGGAGTCAA 36
 |||||

DB

2 TGGGAGTCAA 11

RESULT 11

TA115C11P

LOCUS

DEFINITION

TA115C11P 40 bp DNA linear GSS 13-DEC-2000
 T1 brucei shared genomic DNA clone 115c11, forward sequence,
 genomic survey sequence.
 AL462827
 AL462827.1 GI:11832508

ACCESSION

AL462827

VERSION

AL462827.1 GI:11832508

KEYWORDS

GSS.

SOURCE

ORGANISM

Trypanosoma brucei.
 Trypanosoma brucei.
 Eukaryota, Eukaryota: Kinetoplastida, Trypanosomatidae:
 Trypanosoma.
 1 (bases 1 to 40)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Good, D., Harris, B., El-Sayed, N., Hou, L.,
 McInnis, S.P., Rajandram, M.A. and Barrett, B.G.
 Direct Submission
 Submitted (10-Dec-2000) trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, e-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (IGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 trypanosoma brucei (trypom74 clone) in 1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999)
 Email: nh@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at <http://www.sanger.ac.uk/Genomes/tryb.html>.

Tel: 650 725 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 plasmid 1008027 row: 6
 Class: transposon-tagged

FEATURES

1..40
 Location/Qualifiers

BASE COUNT

12 a 5 c 14 g 9 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pled. No. 9e-04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QUERY

27 TGGGAGTCAA 36
 |||||

DB

2 TGGGAGTCAA 11

RESULT 11

TA115C11P

LOCUS

DEFINITION

TA115C11P 40 bp DNA linear GSS 13-DEC-2000
 T1 brucei shared genomic DNA clone 115c11, forward sequence,
 genomic survey sequence.
 AL462827
 AL462827.1 GI:11832508

ACCESSION

AL462827

VERSION

AL462827.1 GI:11832508

KEYWORDS

GSS.

SOURCE

ORGANISM

Trypanosoma brucei.
 Trypanosoma brucei.
 Eukaryota, Eukaryota: Kinetoplastida, Trypanosomatidae:
 Trypanosoma.
 1 (bases 1 to 40)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Good, D., Harris, B., El-Sayed, N., Hou, L.,
 McInnis, S.P., Rajandram, M.A. and Barrett, B.G.
 Direct Submission
 Submitted (10-Dec-2000) trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, e-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (IGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 trypanosoma brucei (trypom74 clone) in 1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999)
 Email: nh@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at <http://www.sanger.ac.uk/Genomes/tryb.html>.

FEATURES
SOURCE
1. 40
/organism "Typanosoma brucei"
/strain "TRE927"
/db_xref "taxon:6641"
/clone "115c11"

BASE COUNT
G 7 A 11 C 12 G 10 T 1

QUERY MATCH
Post local similarity 24.8% Score 109 DB 17 Length 409
Matches 109 Conservative 09 Mismatches 09 Indels 0 Gaps 0

U9 23 GCAAGGTCGG 40
|||||
db 26 GAAAGTTCAG 45

RESULT 12
BF784672 41 bp mRNA linear EST 12 JAN 2001
LOCUS 53211138.01 NC120000.114 Kozak consensus (Kozak 1986) IMAGC1459300
DEFINITION
BF784672
VERSION BF784672.1 GI:1289739
KEYWORDS
EST
SOURCE house mouse
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
AUTHORS Rat M. Hoffmann, et al. 1997
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: eugene@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNC)
DNA Sequencing by: Inyele Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNC at:
http://image.llnl.gov
Platform: ILM0052 row: 1 column: 01
High quality sequence stop: 47
Location/Qualifiers
1. 41
/organism "Mus musculus"
/strain "EVH/2"
/db_xref "taxon:10096"
/clone "IMAGC:4239460"
/db_host "db100 (FL Phage-resistant)"
/note="Organ: kidney; Vector: pCMV-Sport6; Site: 1; Note:
Site 2: Salt cloned unidirectionally, primer oligo dT.
Average insert size: 177 bp. Inserted by: J.E.
Technologies. Note: this is a NCI/CCAF library."*

BASE COUNT
G 7 A 10 C 20 G 4 T 1

QUERY MATCH
Post local similarity 24.8% Score 109 DB 17 Length 419
Matches 109 Conservative 09 Mismatches 09 Indels 0 Gaps 0

U9 25 GATTGAGTCT 44
|||||
db 20 GATTGAGTCT 29

RESULT 13
AA994992 43 bp mRNA linear EST 27 AUG 1998
LOCUS 569609.31 Sources: NC120000.1 Homo sapiens cDNA clone
DEFINITION

FEATURES
SOURCE
1. 43
/organism "Homo sapiens"
/strain "1460139906"
/db_xref "IMAGC:162752"
/clone "11b" "Sources: NC120000.1"

BASE COUNT
G 9 A 9 C 15 G 10 T 1

QUERY MATCH
Post local similarity 24.8% Score 109 DB 99 Length 439
Matches 109 Conservative 09 Mismatches 09 Indels 0 Gaps 0

U9 15 GATGCTGCA 24
|||||
db 14 CATGCGTCAA 5

RESULT 14
BB854287 43 bp DNA linear GSS 13 JUN 2002
LOCUS 569609.31 5645.2 bp 11.7 kb Human cDNA Insertion 11005
DEFINITION
BB854287
VERSION BB854287.1 GI:21424178
KEYWORDS
GSS
SOURCE Talle cross
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 43)
AUTHORS Alonso, J.M., Leisse, J.L., Barajas, P., Chen, H., Chouk, K., Garbich,
J., Jeske, A., Katus, M., Kim, J.J., Parker, H., Proebst, L., Shum, K.,
Zimmerman, J., and Pickett, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)

FEATURES
SOURCE
1. 43
/organism "Homo sapiens"
/strain "1460139906"
/db_xref "IMAGC:162752"
/clone "11b" "Sources: NC120000.1"

BASE COUNT
G 9 A 9 C 15 G 10 T 1

QUERY MATCH
Post local similarity 24.8% Score 109 DB 99 Length 439
Matches 109 Conservative 09 Mismatches 09 Indels 0 Gaps 0

U9 15 GATGCTGCA 24
|||||
db 14 CATGCGTCAA 5

RESULT 14
BB854287 43 bp DNA linear GSS 13 JUN 2002
LOCUS 569609.31 5645.2 bp 11.7 kb Human cDNA Insertion 11005
DEFINITION
BB854287
VERSION BB854287.1 GI:21424178
KEYWORDS
GSS
SOURCE Talle cross
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 43)
AUTHORS Alonso, J.M., Leisse, J.L., Barajas, P., Chen, H., Chouk, K., Garbich,
J., Jeske, A., Katus, M., Kim, J.J., Parker, H., Proebst, L., Shum, K.,
Zimmerman, J., and Pickett, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)

COMMENT

Contact: Joseph P. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 458 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atg950960.
Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..43

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SAIK_076302.53.45.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/ttn_protocols.html

BASE COUNT

14 a 9 c 9 g 11 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 10; DB 17; Length 43;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATCGGTGAG 25
|||||

DB 32 ATCGGTGAG 41

RESULT 15

BH863967

LOCUS

DEFINITION

SAIK_06605 Arabidopsis thaliana TDNA insertion lines Arabidopsis

thaliana genomic clone SAIK_095005, DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

JOURNAL

UNPUBLISHED (2001)

Contract: Joseph P. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of Atg950960.

Class: TDNA tagged.

Location/Qualifiers

1..45

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SAIK_095005"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

BASE COUNT

10 a 10 c 10 g 15 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 10; DB 17; Length 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGTTGAGCAT 17
|||||

DB 31 CGTTGAGCAT 40

Search completed: April 18, 2003, 04:27:01
Job time : 25195 secs

each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/ttn_protocols.html

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using SW model

Run on: April 17, 2003, 11:32:34 Search time 2046 seconds

(without alignments) 53.038 Million cell updates/sec

Title: US-09-701-394-1

Perfect score: 12

Sequence: 1 accgatggcttgatgacatggg

Scoring table: OLIGO_NUC

Gapop 60.0

Scoring table: Gapext 60.0

Word size: 0

Total number of hits satisfying chosen parameters: 84150

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database: GenEmbl:
1: gb_pa:
2: gb_pg:
3: gb_in:
4: gb_cm:
5: gb_ov:
6: gb_pat:
7: gb_pl:
8: gb_pl:
9: gb_pl:
10: gb_pl:
11: gb_pl:
12: gb_pl:
13: gb_pl:
14: gb_pl:
15: gb_pl:
16: gb_pl:
17: gb_pl:
18: gb_pl:
19: gb_pl:
20: gb_pl:
21: gb_pl:
22: gb_pl:
23: gb_pl:
24: gb_pl:
25: gb_pl:
26: gb_pl:
27: gb_pl:
28: gb_pl:
29: gb_pl:
30: gb_pl:
31: gb_pl:
32: gb_pl:
33: gb_pl:
34: gb_pl:
35: gb_pl:
36: gb_pl:
37: gb_pl:
38: gb_pl:
39: gb_pl:
40: gb_pl:
41: gb_pl:

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	24	57.1	28	6	AA448933	AA448933 Sequence
2	24	57.1	28	6	AA451589	AA451589 Sequence
3	24	57.1	28	6	AA456896	AA456896 Sequence
4	22	52.4	25	6	AA358457	AA358457 Sequence
5	22	52.4	26	6	A57384	A57384 Sequence 21
6	22	52.4	26	6	AA358414	AA358414 Sequence
7	22	52.4	26	6	AA358414	AA358414 Sequence
8	22	52.4	26	6	AA358414	AA358414 Sequence
9	22	52.4	26	6	AA358414	AA358414 Sequence
10	22	52.4	26	6	AA358414	AA358414 Sequence
11	22	52.4	26	6	AA358414	AA358414 Sequence
12	22	52.4	26	6	AA358414	AA358414 Sequence
13	22	52.4	26	6	AA358414	AA358414 Sequence
14	22	52.4	26	6	AA358414	AA358414 Sequence
15	22	52.4	26	6	AA358414	AA358414 Sequence
16	22	52.4	26	6	AA358414	AA358414 Sequence
17	22	52.4	26	6	AA358414	AA358414 Sequence
18	22	52.4	26	6	AA358414	AA358414 Sequence
19	22	52.4	26	6	AA358414	AA358414 Sequence
20	22	52.4	26	6	AA358414	AA358414 Sequence
21	22	52.4	26	6	AA358414	AA358414 Sequence
22	22	52.4	26	6	AA358414	AA358414 Sequence
23	22	52.4	26	6	AA358414	AA358414 Sequence
24	22	52.4	26	6	AA358414	AA358414 Sequence
25	22	52.4	26	6	AA358414	AA358414 Sequence
26	22	52.4	26	6	AA358414	AA358414 Sequence
27	22	52.4	26	6	AA358414	AA358414 Sequence
28	22	52.4	26	6	AA358414	AA358414 Sequence
29	22	52.4	26	6	AA358414	AA358414 Sequence
30	22	52.4	26	6	AA358414	AA358414 Sequence
31	22	52.4	26	6	AA358414	AA358414 Sequence
32	22	52.4	26	6	AA358414	AA358414 Sequence
33	22	52.4	26	6	AA358414	AA358414 Sequence
34	22	52.4	26	6	AA358414	AA358414 Sequence
35	22	52.4	26	6	AA358414	AA358414 Sequence
36	22	52.4	26	6	AA358414	AA358414 Sequence
37	22	52.4	26	6	AA358414	AA358414 Sequence
38	22	52.4	26	6	AA358414	AA358414 Sequence
39	22	52.4	26	6	AA358414	AA358414 Sequence
40	22	52.4	26	6	AA358414	AA358414 Sequence
41	22	52.4	26	6	AA358414	AA358414 Sequence
42	22	52.4	26	6	AA358414	AA358414 Sequence
43	22	52.4	26	6	AA358414	AA358414 Sequence
44	22	52.4	26	6	AA358414	AA358414 Sequence
45	22	52.4	26	6	AA358414	AA358414 Sequence

ALIGNMENTS

RESULT 1
AX448933/C
Sequence 33 from Patent WO226823.
Accession AX448933
Version AX448933.1 GI:21697801
Keywords
Source
Organism
Reference
Authors
Title
battaglini, P., Feder, J. N., Martinez, C., Panathathan, C. S., Westphal, K., Bakken, D. R., Caracci, A., Barber, L. and Forrester, M. G.
A novel human g-protein coupled receptor, huplrm7, expressed highly in spinal cord

JOURNAL Patient: W00226987-A 26-04-APR-2002
 FEATURES Bristol-Myers Squibb Co. (US)
 SOURCE Location/Qualifiers
 1. 28
 /organism "synthetic construct"
 /db_xref "taxon:32640"
 /note "GAGGHH-PVIC Tagmu(R) Probe"
 BASE COUNT 6 a 11 c 3 q 8 t
 ORIGIN

Query Match 57.1% Score 24; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGTGAAGGTCGAGTCAAGCGATT 42
 DB 26 GGTGAAGGTCGAGTCAAGCGATT 4

RESULT 2
 LOCUS AX51589 28 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 28 from Patient W00226987.
 ACCESSION AX51589
 VERSION AX51589.1 GI:2169858
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM artificial sequences
 1
 REFERENCE
 AUTHORS Foster, J.N., Miniet, G., Ramnathan, C.S., Hawken, D.R., Cacace, A.,
 TITLE A novel human T protein coupled receptor, hGPR5, expressed highly
 JOURNAL Patient: W00226987-A 26-04-APR-2002
 FEATURES Bristol-Myers Squibb Co. (US)
 SOURCE Location/Qualifiers
 1. 28
 /organism "synthetic construct"
 /db_xref "taxon:32640"
 /note "GAGGHH-PVIC Tagmu(R) Probe"
 BASE COUNT 6 a 11 c 3 q 8 t
 ORIGIN

Query Match 57.1% Score 24; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGTGAAGGTCGAGTCAAGCGATT 42
 DB 26 GGTGAAGGTCGAGTCAAGCGATT 4

RESULT 4
 LOCUS AX58457 25 bp DNA linear PAT 14-FEB-2002
 DEFINITION Sequence 7 from Patient W00227801.
 ACCESSION AX58457
 VERSION AX58457.1 GI:18675071
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM artificial sequences
 1
 REFERENCE
 AUTHORS Scharm, H.
 TITLE Human serine-threonine kinase
 JOURNAL Patient: W00227801-A 27-10-NOV-2002
 FEATURES MECKE PATENT GmbH (DE)
 SOURCE Location/Qualifiers
 1. 25
 /organism "synthetic construct"
 /db_xref "taxon:32640"
 /note "pTmyc4"
 BASE COUNT 6 a 4 c 10 q 4 t
 ORIGIN

Query Match 52.4% Score 22; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TGAAGGTCGAGTCAAGCGATT 42
 DB 1 TGAAGGTCGAGTCAAGCGATT 22

RESULT 5
 LOCUS A57484 26 bp DNA linear PAT 03-MAR-1998
 DEFINITION Sequence 21 from Patient H0036608.
 ACCESSION A57484
 VERSION A57484.1 GI:3714264
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 1 (bases 1 to 26)
 REFERENCE
 AUTHORS Frey, B.D. and Kuehl, H.
 TITLE Method for the specific amplification and detection of DNA and RNA
 JOURNAL Patient: H0036608-A 21-09-SEP-1996
 FEATURES BOEHRINGER MANNHEIM GmbH (DE)
 COMMENT Other publication JP 9079299 970121.
 SOURCE Location/Qualifiers
 1. 26
 /organism "unidentified"
 /db_xref "taxon:32640"
 BASE COUNT 6 a 4 c 10 q 7 t
 ORIGIN

Query Match 52.4% Score 22; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 22: Conservative 0: Mismatches 9: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 6
 AR028444 26 bp RNA linear PAT 29-SEP-1999
 LOCUS Sequence 6 from Patent us 5858673
 DEFINITION AR028444
 ACCESSION AR028444
 VERSION AR028444.1 GI:5940417
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Price,D.K. and Reidland,C.M.
 TITLE Method for detecting prostate cells
 JOURNAL Patent: US 5858673-A 9 12 JAN-1999;
 FEATURES location/Qualifiers
 source 1..26 /organism="unknown"

BASE COUNT 6 a 3 c 10 g 7 t

ORIGIN
 Query Match 52.4% Score 22 DB 6 Length 26;
 Best Local Similarity 100.0% Pred No 0.033;
 Mismatches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 7
 AR075383 26 bp DNA linear PAT 30-AUG-2000
 LOCUS Sequence 3 from Patent US 6457472
 DEFINITION AR075383
 ACCESSION AR075383
 VERSION AR075383.1 GI:10002193
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Williams,S.K. and Stopeck,A
 TITLE Implants possessing a surface of endothelial cells
 JOURNAL Patent: US 6457472-A 3 28-SEP-1999;
 FEATURES location/Qualifiers
 source 1..26 /organism="unknown"

BASE COUNT 6 a 3 c 10 g 7 t

ORIGIN
 Query Match 52.4% Score 22 DB 6 Length 26;
 Best Local Similarity 100.0% Pred No 0.033;
 Mismatches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 8
 AX015219 26 bp DNA linear PAT 07-SEP-2000
 LOCUS Sequence 1 from Patent WO0561987
 DEFINITION AX015219
 ACCESSION AX015219
 VERSION AX015219.1 GI:19041252
 KEYWORDS
 SOURCE

SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Antel,J.P. and Prat,A.
 TITLE Bradykinin receptor as marker for inflammatory diseases
 JOURNAL Patent: WO 9951987-A 1 14-SEP-1999;
 FEATURES location/Qualifiers
 source 1..26 /organism="synthetic construct"
 /db-acc="E2630"
 /note="GAPDH 5' primer"

BASE COUNT 6 a 3 c 10 g 7 t

ORIGIN
 Query Match 52.4% Score 22 DB 6 Length 26;
 Best Local Similarity 100.0% Pred No 0.033;
 Mismatches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 9
 AX030701 26 bp DNA linear PAT 20-SEP-2000
 LOCUS Sequence 21 from Patent EP0745687.
 DEFINITION AX030701
 ACCESSION AX030701
 VERSION AX030701.1 GI:19278222
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Kuebler,H. and Frey,B.D.
 TITLE Method for the specific amplification and detection of dna and rna
 JOURNAL Patent: EP 0745687-A 21 04-DEC-1996;
 FEATURES location/Qualifiers
 source 1..26 /organism="unidentified"
 /db-acc="E2644"

BASE COUNT 6 a 3 c 10 g 7 t

ORIGIN
 Query Match 52.4% Score 22 DB 6 Length 26;
 Best Local Similarity 100.0% Pred No 0.033;
 Mismatches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 21 TGAAGTGGAGTCAACGATT 42
 |||
 DB 1 TGAAGTGGAGTCAACGATT 22

RESULT 10
 AX166503 26 bp DNA linear PAT 23-JUN-2001
 LOCUS Sequence 158 from Patent WO0136478.
 DEFINITION AX166503
 ACCESSION AX166503
 VERSION AX166503.1 GI:14546851
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Baillouet,D.-G., Muttero,J.J., Chin,X., Miao,R.K., Haley,D.A. and
 Hoyle,B.J.
 TITLE Methods and compositions relating to bactericidal/permeability
 increasing factor like polypeptides and polynucleotides
 JOURNAL Patent: WO 0136478 A 158 25-MAY 2001;
 INVENO, INC. (US)

FEATURES

SOURCE

Location/Qualifiers
1..26
/organism "Synthetic Construct"
/db_xref "taxon:32630"
/note "Chemically Synthesized"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.043;

Matches 22; Conservative 0; Mismatches 0; Indels 0;
Db 1 TGAAGTGGAGTCAACGGATT 22

RESULT 11
AX174821
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX174821
Sequence 49 from Patent WO0144282.
AX174821.1 GI:14598417
SYNTHETIC CONSTRUCT.
SYNTHETIC CONSTRUCT.
artificial sequences.

REFERENCE
1 (bases 1 to 26)
Brod, J.C. and Gold, R.A.
TITLE
JOURNAL
AUTHORS

Polypeptides, encoding nucleic acids and methods of use
Patient: WO 0144282-A 49 21-JUN-2001;
The Burham Institute (US)

FEATURES
SOURCE
1..26
Location/Qualifiers

/organism "Synthetic Construct"
/db_xref "taxon:32630"
/note "Synthetic primer"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.043;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TGAAGTGGAGTCAACGGATT 22

RESULT 12
AX175502
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX175502
Sequence 41 from Patent WO0144443.
AX175502.1 GI:14598445
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 26)
Whitney, A., Iwakochi, P.M., Jones, G., and Kamshaw, H.
TITLE
JOURNAL
AUTHORS

Cytochrome P450c17 and related proteins
Patient: WO 0144443-A 41 21-JUN-2001;
Cytochrome Inc. (VA)

FEATURES
SOURCE
1..26
Location/Qualifiers

/organism "Homo sapiens"
/db_xref "taxon:32630"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;

Best Local Similarity 100.0%; Prod. No. 0.043;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TGAAGTGGAGTCAACGGATT 22

RESULT 14
AX175510
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX175510
Sequence 49 from Patent WO0144443.
AX175510.1 GI:14598454
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 26)
Whitney, A., Iwakochi, P.M., Jones, G., and Kamshaw, H.
TITLE
JOURNAL
AUTHORS

Cytochrome P450c17 and related proteins
Patient: WO 0144443-A 49 21-JUN-2001;
Cytochrome Inc. (VA)

FEATURES
SOURCE
1..26
Location/Qualifiers

/organism "Homo sapiens"
/db_xref "taxon:32630"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.043;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TGAAGTGGAGTCAACGGATT 22

RESULT 14
AX298289
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX298289
Sequence 5 from Patent WO0184768.
AX298289.1 GI:12128406
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1
Parker, K. and Schram, B.
TITLE
JOURNAL
AUTHORS

Setine-threonine kinase
Patient: WO 0184768-A 5 08 NOV 2001;
MERCK PATENT GmbH (DE)

FEATURES
SOURCE
1..26
Location/Qualifiers

/organism "Synthetic Construct"
/db_xref "taxon:32630"
/note "Primer"

BASE COUNT 6 a 3 c 10 g 7 t
ORIGIN

Query Match 52.4%; Score 22; DB 6; Length 26;
Best Local Similarity 100.0%; Prod. No. 0.043;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TGAAGTGGAGTCAACGGATT 22

RESULT 15
AX298289
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX298289
Sequence 5 from Patent WO0184768.
AX298289.1 GI:12128406
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AX300719
 LOCUS AX300719 26 bp DNA linear PAT 30 NOV 2001
 DEFINITION Sequence 5 from Patent W0185954.
 ACCESSION AX300719
 VERSION AX300719.1 GI:17382022
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 1 artificial sequences.
 REFERENCE
 1
 AUTHORS Schart, B. and Dieckhoff, K.
 TITLE Serine-threonine Kinase-3
 JOURNAL Patent: WO 0185954-A 5 15-NOV-2001;
 MERCK PATENT GmbH (DE)
 FEATURES
 1
 1..26
 location/qualifiers
 /organism="synthetic construct"
 /db_xref="taxon:22630"
 /note="Primer 4"
 BASE COUNT 6 a 3 c 10 g 7 t
 ORIGIN
 Query Match 52.1%, Score 22, DB 6, Length 26;
 Best Local Similarity 100.0%, Pred. No. 0.033;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 21 TCAAGCTGGAGTCAACGGATT 42
 ID 1 TCAAGCTGGAGTCAACGGATT 22

Search completed: April 17, 2003, 20:40:56
 Job time : 23049 secs

PT Novel G protein-coupled receptor, HSPRBM7 polypeptide, useful for
PT treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative
PT colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,
PT osteoarthritis

XX Example 4: Page 77; 146pp; English.

XX The present invention relates to the isolation of a novel human
CC G-protein coupled receptor (GPCR) (HSPRBM7), and the polynucleotide
CC sequence encoding it. The HSPRBM7 polypeptide and polynucleotide
CC are useful for preventing, treating or ameliorating a disease,
CC disorder or condition related to the colon, brain, ovaries, thymus,
CC lungs or immune system. They are particularly useful for the
CC treatment or prevention of cancers, immune disorders, neurological
CC disorders, and diseases related to the brain, ovaries, thymus or
CC lungs. The polynucleotide sequence is useful for diagnosing or
CC determining susceptibility to infections such as bacterial, fungal,
CC protozoan and viral infections, particularly HIV and HTV 2). The present sequence
CC human immunodeficiency virus (HIV or HTV 2). The present sequence
CC represents a probe used for DNA encoding human GPCR
CC (D-lysine(337)-3-phosphate, 3-hydroxyphosphate) in the examples of the
CC present invention.

CC Sequence 28 BP; 6 A; 11 G; 3 G; 8 T; 0 other:

Query Match 57.1%; Score 24; DE 24; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00026; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 GGTGAAGTGGAGTCAACGATT 42

26 GGTGAAGTGGAGTCAACGATT 3

RESULT 4

ABR4820/C

ABR4820 standard; DNA: 26 BP.

AC ABR4820;

XX 13-AUG-2002 (first entry)

DE Human glyceraldehyde phosphate dehydrogenase for probe.

XX Human: PCR; ss; G protein coupled receptor, HSPRBM7; spinal chord;

XX spinal chord-related disorder, breast cancer, neoplastic disease;

XX brain disorder, leukodystrophy, myeloma; immunological disorder; probe;

XX cholesteatoma; Grave's disease, osteoarthritis, asthma,

XX neurological disorder, dementia, depression, Alzheimer's disease,

XX Down's syndrome, epilepsy; intracellular calcium level; NFAT;

XX nuclear factor activation of transcription element.

XX Homo sapiens.

XX W0200226927-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001WO-US30351.

XX 27-SEP-2000; 2000US-235731P.

XX 14-FEB-2001; 2001US-268280P.

XX 28-AUG-2001; 2001US-315412P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Battaglini P, Feder JN, Muttler G, Ramasathan CS, Westphal F,

XX Harker RP, Caruso A, Barber L, Kornacker MG;

XX WPI; 2002-435195/46.

XX Novel human G protein coupled receptor BMT7 (HSPRBM7) polypeptide,
PI useful for modulators of HSPRBM7 activity that are useful for treating

PT leukemia, rheumatoid arthritis, chronic disease, epilepsy, dementia,
PT depression

XX Example 4; Page 77; 170pp; English.

XX The invention relates to an isolated polypeptide (1) comprising amino
CC acid sequence that is at least 90% identical to a polypeptide fragment of
CC a fully defined human G protein-coupled receptor BMT7 (HSPRBM7)
CC polypeptide, or variant, allelic variant or species homologue.
CC Also included are polynucleotides encoding the above polypeptides,
CC expression vectors, host cells, and antibodies and modulators
CC of HSPRBM7. HSPRBM7 and its polynucleotide are useful for diagnosis,
CC prevention, treating or ameliorating a medical condition, e.g. a disease,
CC disorder, or a condition related to brain, breast, gastrointestinal or
CC muscular/skeletal systems, such that thalamus, corpus callosum,
CC cerebellum, caudate nucleus, amygdala, substantia nigra,
CC hippocampus, brain, breast, colon, and disorders related to spinal
CC breast cancer, neoplastic diseases, and disorders related to spinal
CC chord and brain. An antagonist or inhibitor of (1) identified using (1)
CC is useful for treating a neoplastic disorder such as leukemia, myeloma,
CC immunological disorders such as rheumatoid arthritis, chronic disease,
CC osteoarthritis, asthma, neurological disorders such as dementia,
CC depression, Alzheimer's disease, Down's syndrome and epilepsy.

XX HSPRBM7, its polynucleotide and agonists or antagonists of the

XX polypeptide are useful for modulating intracellular calcium levels,

XX modulating other specific signalling pathways and modulating nuclear

XX factor activation of transcription (NFAT) element associated signalling

XX pathways. The present sequence is a PCR probe used in an experiment to

XX quantitate HSPRBM7 mRNA.

XX Sequence 28 BP; 6 A; 11 G; 3 G; 8 T; 0 other:

Query Match 57.1%; Score 24; DE 24; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00026;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 GGTGAAGTGGAGTCAACGATT 42

26 GGTGAAGTGGAGTCAACGATT 3

RESULT 5

ABR70642/C

ABR70642 standard; DNA: 28 BP.

AC ABR70642;

XX 16-JUN-2002 (first entry)

XX GAPDH probe.

XX Human: G-protein coupled receptor; HSPRBM7; small intestine; colon;

XX testis; cancer; PCR; primer; ss.

XX Homo sapiens.

XX W0200226927-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001WO-US30614.

XX 27-SEP-2000; 2000US-236032P.

XX 19-JUL-2001; 2001US-406040P.

XX 28-AUG-2001; 2001US-315412P.

XX (PRIM) BRISTOL-MYERS SQUIBB CO.

XX Feder JN, Muttler G, Ramasathan CS, Hawken JR, Caruso A, Barber L,

XX Kornacker MG;

XX WPI; 2002-435195/41.

OJ 21 TGAAGTGGAGTCAACGGATT 42
 1 TGAAGTGGAGTCAACGGATT 22

RESULT 8
 AAT29240
 ID AAT29240 standard; DNA; 26 BP.

AC AAT29240
 DT 16-JUL-1996 (first entry)

DE Glyceraldehyde-3-phosphate-dehydrogenase sense primer.
 XX 31-mer, 3'-GGG-5' (the 31-mer is hydrophobic; interlockin-8;
 KM sense primer; antisense primer; polymerase chain reaction; PCR;
 KM CagA; CagA; CagA; CagA; CagA; CagA; CagA; CagA; CagA; CagA;
 KM antisense oligonucleotide; treatment; prevention; diagnosis;
 KM attenuation; vaccine; ss

XX Synthetic.
 OS
 XX W09632925-A1
 XX PD 02-MAV-1996.
 XX PF 20-OCT-1996. 9460-nel4659

XX 21-CCF-1994; 940S-0327494.
 XX (VVA-) HIV VANDPRIT
 XX FA
 XX PI Blaser MJ, Sharma SA, Tummuru MKR;

XX WPI: 1996-230633/22.
 XX DR
 XX PT DNA encoding Helicobacter pylori CagA and CagE antigens;
 PT F-10-11-12-13-14-15-16-17-18-19-20-21-22-23-24-25-26-27-28-29-30-31-32-33-34-35-36-37-38-39-40-41-42-43-44-45-46-47-48-49-50-51-52-53-54-55-56-57-58-59-60-61-62-63-64-65-66-67-68-69-70-71-72-73-74-75-76-77-78-79-80-81-82-83-84-85-86-87-88-89-90-91-92-93-94-95-96-97-98-99-100-101-102-103-104-105-106-107-108-109-110-111-112-113-114-115-116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000-1001-1002-1003-1004-1005-1006-1007-1008-1009-1010-1011-1012-1013-1014-1015-1016-1017-1018-1019-1020-1021-1022-1023-1024-1025-1026-1027-1028-1029-1030-1031-1032-1033-1034-1035-1036-1037-1038-1039-1040-1041-1042-1043-1044-1045-1046-1047-1048-1049-1050-1051-1052-1053-1054-1055-1056-1057-1058-1059-1060-1061-1062-1063-1064-1065-1066-1067-1068-1069-1070-1071-1072-1073-1074-1075-1076-1077-1078-1079-1080-1081-1082-1083-1084-1085-1086-1087-1088-1089-1090-1091-1092-1093-1094-1095-1096-1097-1098-1099-1100-1101-1102-1103-1104-1105-1106-1107-1108-1109-1110-1111-1112-1113-1114-1115-1116-1117-1118-1119-1120-1121-1122-1123-1124-1125-1126-1127-1128-1129-1130-1131-1132-1133-1134-1135-1136-1137-1138-1139-1140-1141-1142-1143-1144-1145-1146-1147-1148-1149-1150-1151-1152-1153-1154-1155-1156-1157-1158-1159-1160-1161-1162-1163-1164-1165-1166-1167-1168-1169-1170-1171-1172-1173-1174-1175-1176-1177-1178-1179-1180-1181-1182-1183-1184-1185-1186-1187-1188-1189-1190-1191-1192-1193-1194-1195-1196-1197-1198-1199-1200-1201-1202-1203-1204-1205-1206-1207-1208-1209-1210-1211-1212-1213-1214-1215-1216-1217-1218-1219-1220-1221-1222-1223-1224-1225-1226-1227-1228-1229-1230-1231-1232-1233-1234-1235-1236-1237-1238-1239-1240-1241-1242-1243-1244-1245-1246-1247-1248-1249-1250-1251-1252-1253-1254-1255-1256-1257-1258-1259-1260-1261-1262-1263-1264-1265-1266-1267-1268-1269-1270-1271-1272-1273-1274-1275-1276-1277-1278-1279-1280-1281-1282-1283-1284-1285-1286-1287-1288-1289-1290-1291-1292-1293-1294-1295-1296-1297-1298-1299-1300-1301-1302-1303-1304-1305-1306-1307-1308-1309-1310-1311-1312-1313-1314-1315-1316-1317-1318-1319-1320-1321-1322-1323-1324-1325-1326-1327-1328-1329-1330-1331-1332-1333-1334-1335-1336-1337-1338-1339-1340-1341-1342-1343-1344-1345-1346-1347-1348-1349-1350-1351-1352-1353-1354-1355-1356-1357-1358-1359-1360-1361-1362-1363-1364-1365-1366-1367-1368-1369-1370-1371-1372-1373-1374-1375-1376-1377-1378-1379-1380-1381-1382-1383-1384-1385-1386-1387-1388-1389-1390-1391-1392-1393-1394-1395-1396-1397-1398-1399-1400-1401-1402-1403-1404-1405-1406-1407-1408-1409-1410-1411-1412-1413-1414-1415-1416-1417-1418-1419-1420-1421-1422-1423-1424-1425-1426-1427-1428-1429-1430-1431-1432-1433-1434-1435-1436-1437-1438-1439-1440-1441-1442-1443-1444-1445-1446-1447-1448-1449-1450-1451-1452-1453-1454-1455-1456-1457-1458-1459-1460-1461-1462-1463-1464-1465-1466-1467-1468-1469-1470-1471-1472-1473-1474-1475-1476-1477-1478-1479-1480-1481-1482-1483-1484-1485-1486-1487-1488-1489-1490-1491-1492-1493-1494-1495-1496-1497-1498-1499-1500-1501-1502-1503-1504-1505-1506-1507-1508-1509-1510-1511-1512-1513-1514-1515-1516-1517-1518-1519-1520-1521-1522-1523-1524-1525-1526-1527-1528-1529-1530-1531-1532-1533-1534-1535-1536-1537-1538-1539-1540-1541-1542-1543-1544-1545-1546-1547-1548-1549-1550-1551-1552-1553-1554-1555-1556-1557-1558-1559-1560-1561-1562-1563-1564-1565-1566-1567-1568-1569-1570-1571-1572-1573-1574-1575-1576-1577-1578-1579-1580-1581-1582-1583-1584-1585-1586-1587-1588-1589-1590-1591-1592-1593-1594-1595-1596-1597-1598-1599-1600-1601-1602-1603-1604-1605-1606-1607-1608-1609-1610-1611-1612-1613-1614-1615-1616-1617-1618-1619-1620-1621-1622-1623-1624-1625-1626-1627-1628-1629-1630-1631-1632-1633-1634-1635-1636-1637-1638-1639-1640-1641-1642-1643-1644-1645-1646-1647-1648-1649-1650-1651-1652-1653-1654-1655-1656-1657-1658-1659-1660-1661-1662-1663-1664-1665-1666-1667-1668-1669-1670-1671-1672-1673-1674-1675-1676-1677-1678-1679-1680-1681-1682-1683-1684-1685-1686-1687-1688-1689-1690-1691-1692-1693-1694-1695-1696-1697-1698-1699-1700-1701-1702-1703-1704-1705-1706-1707-1708-1709-1710-1711-1712-1713-1714-1715-1716-1717-1718-1719-1720-1721-1722-1723-1724-1725-1726-1727-1728-1729-1730-1731-1732-1733-1734-1735-1736-1737-1738-1739-1740-1741-1742-1743-1744-1745-1746-1747-1748-1749-1750-1751-1752-1753-1754-1755-1756-1757-1758-1759-1760-1761-1762-1763-1764-1765-1766-1767-1768-1769-1770-1771-1772-1773-1774-1775-1776-1777-1778-1779-1780-1781-1782-1783-1784-1785-1786-1787-1788-1789-1790-1791-1792-1793-1794-1795-1796-1797-1798-1799-1800-1801-1802-1803-1804-1805-1806-1807-1808-1809-1810-1811-1812-1813-1814-1815-1816-1817-1818-1819-1820-1821-1822-1823-1824-1825-1826-1827-1828-1829-1830-1831-1832-1833-1834-1835-1836-1837-1838-1839-1840-1841-1842-1843-1844-1845-1846-1847-1848-1849-1850-1851-1852-1853-1854-1855-1856-1857-1858-1859-1860-1861-1862-1863-1864-1865-1866-1867-1868-1869-1870-1871-1872-1873-1874-1875-1876-1877-1878-1879-1880-1881-1882-1883-1884-1885-1886-1887-1888-1889-1890-1891-1892-1893-1894-1895-1896-1897-1898-1899-1900-1901-1902-1903-1904-1905-1906-1907-1908-1909-1910-1911-1912-1913-1914-1915-1916-1917-1918-1919-1920-1921-1922-1923-1924-1925-1926-1927-1928-1929-1930-1931-1932-1933-1934-1935-1936-1937-1938-1939-1940-1941-1942-1943-1944-1945-1946-1947-1948-1949-1950-1951-1952-1953-1954-1955-1956-1957-1958-1959-1960-1961-1962-1963-1964-1965-1966-1967-1968-1969-1970-1971-1972-1973-1974-1975-1976-1977-1978-1979-1980-1981-1982-1983-1984-1985-1986-1987-1988-1989-1990-1991-1992-1993-1994-1995-1996-1997-1998-1999-2000-2001-2002-2003-2004-2005-2006-2007-2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025-2026-2027-2028-2029-2030-2031-2032-2033-2034-2035-2036-2037-2038-2039-2040-2041-2042-2043-2044-2045-2046-2047-2048-2049-2050-2051-2052-2053-2054-2055-2056-2057-2058-2059-2060-2061-2062-2063-2064-2065-2066-2067-2068-2069-2070-2071-2072-2073-2074-2075-2076-2077-2078-2079-2080-2081-2082-2083-2084-2085-2086-2087-2088-2089-2090-2091-2092-2093-2094-2095-2096-2097-2098-2099-2100-2101-2102-2103-2104-2105-2106-2107-2108-2109-2110-2111-2112-2113-2114-2115-2116-2117-2118-2119-2120-2121-2122-2123-2124-2125-2126-2127-2128-2129-2130-2131-2132-2133-2134-2135-2136-2137-2138-2139-2140-2141-2142-2143-2144-2145-2146-2147-2148-2149-2150-2151-2152-2153-2154-2155-2156-2157-2158-2159-2160-2161-2162-2163-2164-2165-2166-2167-2168-2169-2170-2171-2172-2173-2174-2175-2176-2177-2178-2179-2180-2181-2182-2183-2184-2185-2186-2187-2188-2189-2190-2191-2192-2193-2194-2195-2196-2197-2198-2199-2200-2201-2202-2203-2204-2205-2206-2207-2208-2209-2210-2211-2212-2213-2214-2215-2216-2217-2218-2219-2220-2221-2222-2223-2224-2225-2226-2227-2228-2229-2230-2231-2232-2233-2234-2235-2236-2237-2238-2239-2240-2241-2242-2243-2244-2245-2246-2247-2248-2249-2250-2251-2252-2253-2254-2255-2256-2257-2258-2259-2260-2261-2262-2263-2264-2265-2266-2267-2268-2269-2270-2271-2272-2273-2274-2275-2276-2277-2278-2279-2280-2281-2282-2283-2284-2285-2286-2287-2288-2289-2290-2291-2292-2293-2294-2295-2296-2297-2298-2299-2300-2301-2302-2303-2304-2305-2306-2307-2308-2309-2310-2311-2312-2313-2314-2315-2316-2317-2318-2319-2320-2321-2322-2323-2324-2325-2326-2327-2328-2329-2330-2331-2332-2333-2334-2335-2336-2337-2338-2339-2340-2341-2342-2343-2344-2345-2346-2347-2348-2349-2350-2351-2352-2353-2354-2355-2356-2357-2358-2359-2360-2361-2362-2363-2364-2365-2366-2367-2368-2369-2370-2371-2372-2373-2374-2375-2376-2377-2378-2379-2380-2381-2382-2383-2384-2385-2386-2387-2388-2389-2390-2391-2392-2393-2394-2395-2396-2397-2398-2399-2400-2401-2402-2403-2404-2405-2406-2407-2408-2409-2410-2411-2412-2413-2414-2415-2416-2417-2418-2419-2420-2421-2422-2423-2424-2425-2426-2427-2428-2429-2430-2431-2432-2433-2434-2435-2436-2437-2438-2439-2440-2441-2442-2443-2444-2445-2446-2447-2448-2449-2450-2451-2452-2453-2454-2455-2456-2457-2458-2459-2460-2461-2462-2463-2464-2465-2466-2467-2468-2469-2470-2471-2472-2473-2474-2475-2476-2477-2478-2479-2480-2481-2482-2483-2484-2485-2486-2487-2488-2489-2490-2491-2492-2493-2494-2495-2496-2497-2498-2499-2500-2501-2502-2503-2504-2505-2506-2507-2508-2509-2510-2511-2512-2513-2514-2515-2516-2517-2518-2519-2520-2521-2522-2523-2524-2525-2526-2527-2528-2529-2530-2531-2532-2533-2534-2535-2

CC activity and screening for agents that treat inflammatory diseases. The
 CC diseases can be multiple sclerosis, rheumatoid arthritis,
 CC osteoarthritis, Crohn's disease, ulcerative colitis or lupus.
 CC erythema multiforme, disseminated. The marker avoids the use conventional
 CC techniques, which can be more expensive and time-consuming. Sequences
 CC AA23133-114 represent G3PDH primers.
 XX
 SQ Sequence 26 BP; 6 A; 3 C; 10 G; 7 T; 0 other;
 Query Match 52.48, Score 22, DP 20, Length 26;
 Best Local Similarity 100.0%; Pred No. 0.0037;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0Y 21 TGAAGCTCGAGTCAAGCAT 42
 1 TGAAGCTCGAGTCAAGCAT 22
 Db
 RESULT 13
 AA21557
 ID AA21557 standard; DNA; 26 BP.
 XX
 AC AA21557;
 XX
 DE 01-DEC-1999 (first entry)
 XX
 DE 5' PCR primer used for amplification of G3PDH gene.
 XX
 KM G3PDH: gamma interferon; smooth muscle cell proliferation;
 KM intimal thickening; thrombosis; vascular graft; endothelial cell; valve;
 KM genetically modified; cardiovascular graft; artificial blood vessel;
 KM arteriosclerosis; medial arteriosclerosis; heart failure; heart failure;
 KM arterial aneurysm; organ failure; ischemia; blood clot; thrombin; ss;
 KM G173331-1-lyb-3-phosphate-4-lyb-3-phosphate.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5957972-A.
 XX
 PD 28-SEP-1999.
 XX
 XX 23-JAN-1997; 97US-0/8/902.
 XX
 PE 26-JAN-1999; 96US-0010616.
 XX
 PR 29-SEP-1992; 92US-0952474.
 XX
 PA (AR12-) ARIZONA BOARD OF HEALTH.
 XX
 PI Stopcock A, Williams SK;
 XX
 DR WPI; 1999-070744/48
 XX
 PT Preventing smooth muscle cell proliferation; intimal thickening and
 PT thrombosis at the site of vascular grafts.
 XX
 XX
 PS Example 1, Column 13, 15pp, English.
 XX
 CC For primers AA21557 and 559, used to amplify the glyceraldehyde-
 CC 3-phosphate dehydrogenase (G3PDH) gene. G3PDH is used in the method of
 CC the invention, which involves preventing smooth muscle cell
 CC proliferation, intimal thickening and thrombosis at the site of vascular
 CC grafts. The method involves using implants coated with a monolayer of
 CC endothelial cells genetically engineered to express therapeutic agents
 CC (especially gamma interferon) that limit proliferation of smooth muscle
 CC cells. The method may be used to produce cardiovascular grafts
 CC (e.g. artificial blood vessels and valves) for the treatment of
 CC arteriosclerosis (such as atherosclerosis and medial arteriosclerosis),
 CC heart failure, renal failure, arterial aneurysms, organ failure and
 CC other conditions that require vascular bypasses to restore blood flow to
 CC areas of ischemia. The presence of the endothelial cells prevents the
 CC formation of blood clots (thrombosis) on vascular grafts because the
 CC thrombin circulating in the patient's blood does not come into contact

CC with the artificial material of the graft (only the endothelial cells
 CC contact the thrombin which does not cause clotting).
 XX
 SQ Sequence 26 BP; 6 A; 3 C; 10 G; 7 T; 0 other;
 Query Match 52.48, Score 22, DP 20, Length 26;
 Best Local Similarity 100.0%; Pred No. 0.0037;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0Y 21 TGAAGCTCGAGTCAAGCAT 42
 1 TGAAGCTCGAGTCAAGCAT 22
 Db
 RESULT 14
 AAX21362
 ID AAX21362 standard; DNA; 26 BP.
 XX
 AC AAX21362;
 XX
 DE 21-MAY-1999 (first entry)
 XX
 DE Prime HGS for G3PDH gene.
 XX
 KM Human; BAI1; brain; cancer; drug; diagnosis; prevention; treatment;
 KM primer; PCR; amplification; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX 191022766-A.
 XX
 FE 09 FEB-1999.
 XX
 XX 16-JUN-1997; 97JP-0176485.
 XX
 PE 23-MAY-1997; 97JP-0150460
 XX
 XX (SAKA) OTSUKA PHARM CO LTD.
 XX
 PA WPI; 1999-183823/16.
 XX
 DR New human BAI gene - is expressed in brain plays important role in
 DR cancer formation
 XX
 PT New human BAI gene - is expressed in brain plays important role in
 PT cancer formation
 XX
 PS Example 3, Page 16; 62pp; Japanese.
 XX
 CC Primers AAX21362-X21363 were used to PCR amplify a fragment of the G3PDH
 CC (glyceraldehyde-3-phosphate dehydrogenase) gene as a control sequence
 CC for analysis of BAI gene expression in blots. The BAI genes
 CC (AAX21355-X21357) are expressed specifically in the brain and play an
 CC important role in cancer formation in the brain. The BAI proteins can be
 CC used in drug compositions to diagnose, prevent or treat such cancers.
 XX
 SQ Sequence 26 BP; 6 A; 3 C; 10 G; 7 T; 0 other;
 Query Match 52.48, Score 22, DP 20, Length 26;
 Best Local Similarity 100.0%; Pred No. 0.0037;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 0Y 21 TGAAGCTCGAGTCAAGCAT 42
 1 TGAAGCTCGAGTCAAGCAT 22
 Db
 RESULT 15
 AAX01679
 ID AAX01679 standard; DNA; 26 BP.
 XX
 AC AAX01679;
 XX
 DE 01-APR-1999 (first entry)
 XX

RESULT 2

US-09-787-902A-3

Sequence 9, Application US/98851135

Patent No. 5858674

GENERAL INFORMATION:

APPLICANT: Pitco, Douglas K.

APPLICANT: Toland, Chris M.

TITLE OF INVENTION: METHOD FOR DETECTING PROSTATE CELLS

NUMBER OF SEQUENCES: 12

ADDRESS: Ernest B. Lipscomb (Bell)

ADDRESS: Ernest B. Lipscomb (Bell) Solter 1P Group of

ADDRESS: Alston & Bird)

SHEET: Post office drawer 44099

CITY: Charlott

STATE: NC

COUNTRY: US

ZIP: 28244-4009

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,135

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lipscomb III, Ernest B.

REGISTRATION NUMBER: 24,734

REFERENCE/INVENT NUMBER: 815-21

TELECOMMUNICATION INFORMATION:

TELEPHONE: 704 331 6000

TELEFAX: 702 334 2014

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

FEATURE: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: 4 base "5'ggttgccttc" within sequence

DISCUSSION: (Glntr G4PDH5)

US-09-787-902A-3

Query Match 52.4% Score 22 DB 2 Length 26
 Host Local Similarity 100.0% Prod. No. 0.00038
 Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 21 TGAAGTGGAGTCAACGAAATT 42
 DB 1 TGAAGTGGAGTCAACGAAATT 22

US-09-787-902A-3
 Sequence 9, Application US/98797902A

Patent No. 5957972

GENERAL INFORMATION:

APPLICANT: Williams, Stuart K.

APPLICANT: Stopcock, Allison

TITLE OF INVENTION: Improved implants possessing a Suria

TITLE OF INVENTION: Co of Endothelial Cells Genetically Modified to

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: Anticito Institute

STREET: 2929 E. Broadway Blvd.

CITY: Tucson

STATE: AZ

COUNTRY: U.S.A.

ZIP: 85716

COMPUTER READABLE FORM:
 MEDIUM TYPE: diskette, 3.5 inch, 1.44mb storage

COMPUTER: IBM compatible pc

OPERATING SYSTEM: Windows 3.1

SOFTWARE: word perfect 6.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,902A

FILING DATE: 23-JAN-97

CLASSIFICATION: 623

PRIOR APPLICATION DATA:

AFFILIATION NUMBER: 60701-610, 627953, 474

FILING DATE: 26-JAN-96, 24-SEP-92

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

FEATURE: linear

US-08-787-902A-3

Query Match 52.4% Score 22 DB 2 Length 26
 Host Local Similarity 100.0% Prod. No. 0.00038
 Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 21 TGAAGTGGAGTCAACGAAATT 42
 DB 1 TGAAGTGGAGTCAACGAAATT 22

US-09-744-700-13
 Sequence 13, Application US/99241700

Patent No. 6265194

GENERAL INFORMATION:

APPLICANT: Nezu, Jun-ichi

APPLICANT: Oku, Asuka

TITLE OF INVENTION: NOVEL, SERINE THREONINE KINASE GENE

FILE REFERENCE: 06501/034001

CURRENT APPLICATION NUMBER: US/99/444,700

CURRENT FILING DATE: 1999-06-25

EARLIER APPLICATION NUMBER: F01/3197/0485

EARLIER FILING DATE: 1997-12-25

EARLIER FILING DATE: 1996-12-27

FASLIER FILING DATE: 1996-12-27

FASLIER FILING DATE: 1996-12-27

FASLIER FILING DATE: 1996-12-27

FASLIER FILING DATE: 1996-12-27

FASLIER FILING DATE: 1996-12-27

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FASLIER FILING DATE: 1996-12-27

FASLIER FILING DATE: 1996-12-27

FASLIER FILING DATE: 1996-12-27

FASLIER FILING DATE: 1996-12-27

TITLE OF INVENTION: LIPASE ENZYME AND COMPOSITIONS AND METHODS FOR THEIR USE
TITLE OF INVENTION: IN IMMEDIATE HYPOGLYCEMIA AND PROTEIN AND GENE THERAPIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Atcoia Rd. 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/08/985,492
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fehner Ph.D., Paul F.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: A2592-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ. ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc - "oligonucleotide"
US-08-985-492-30
Query Match 52.48; Score 22; DB 4; Length 26;
Best Local Similarity 100.0%; Freq. No. 0 00038;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TGAAGTCGAGTCACGAGATT 22
QY 21 TGAAGTCGAGTCACGAGATT 42
|||||
PCT-US95-13659-5
RESULT 6
Sequence 5, Application PC/TUS9513659
GENERAL INFORMATION:
APPLICANT: Ellsner, Martin I.
APPLICANT: Tumurtu, Mutall K R.
AFFILIANT: Statia, Suley A.
TITLE OF INVENTION: Cystic and cystic Cystic and
TITLE OF INVENTION: Polystyrene Methods and Compositions
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEDRIL & ROSENBERG, P.C.
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 303-3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13659
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Spatt, Gwendolyn D.

REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 2002,029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-13659-5
Query Match 52.48; Score 22; DB 5; Length 26;
Best Local Similarity 100.0%; Freq. No. 0 00038;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TGAAGTCGAGTCACGAGATT 22
QY 21 TGAAGTCGAGTCACGAGATT 42
|||||
RESULT 7
US-08-937-063-1
Sequence 1, Application US/08937063
Patent No. 6187534
GENERAL INFORMATION:
APPLICANT: STROM, TERRY H.
APPLICANT: VASCONCELOS, LAURO
AFFILIANT: 30 HATHAWAY, MAHLEMAN
TITLE OF INVENTION: METHODS OF EVALUATING TRANSPLANT
TITLE OF INVENTION: REJECTION
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: HATHAWAY, JERRY, SMITH & REYNOLDS
STREET: TWO MILLITIA DRIVE
CITY: LEXINGTON
STATE: MASSACHUSETTS
COUNTRY: UNITED STATES
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/08/937,063
FILING DATE: 24-Sep-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRANAMIN, PATRICIA
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: 613697-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-937-063-1
Query Match 47.68; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Freq. No. 0 0056;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 19 GGTGAAGTCGAGTCACG 38
QY 19 GGTGAAGTCGAGTCACG 38
|||||
DB 1 GGTGAAGTCGAGTCACG 20

RESULT 8

US-08-188-444A-13
Sequence 13, Application US/08188434A
Patient No. 5639606
GENERAL INFORMATION:
APPLICANT: Willey, James C.
TITLE OF INVENTION: Method for Quantitative Measurement of
TITLE OF INVENTION: Gene Expression Using Multi-Plex Competitive Reverse
TITLE OF INVENTION: Transcriptase Polymerase Chain Reaction
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Emu, Schaub, & Porcello Co.,
ADDRESS: L.P.A.
STREET: One Squarto, Suite 1980
CITY: Toledo
STATE: Ohio
ZIP: 43604
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: pc-ips/ms-dos
SOFTWARE: Paton to Release #1.9, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08188434A
FILING DATE: 28-Jan-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/043,390
FILING DATE: 06-Apr-1993
ATTORNEY/AGENT INFORMATION:
NAME: Martineau, Catherine R.
REGISTRATION NUMBER: 41,854
REFERENCE/ATTORNEY NUMBER: 34205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (419) 243-1294
TELEFAX: (419) 243-8502
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: liver
PUBLICATION INFORMATION:
AUTHORS: Tokumura, K.
AUTHORS: Nakamura, Y.
AUTHORS: Sakata, K.
AUTHORS: Fujimoto, K.
AUTHORS: Ohkubo, M.
AUTHORS: Sawada, K.
AUTHORS: Sakiyama, S.
TITLE: Enhanced expression of a
TITLE: glyceraldehyde-3-phosphate dehydrogenase gene in
TITLE: human lung cancers
JOURNAL: Cancer Res.
VOLUME: 47
PAGES: 5616-5619
DATE: SUMMER-1990
RELEVANT RESIDUES IN SEQ ID NO: 13: FROM 1 TO 24
US-08-188-444A-13

Query Match 42.9%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Freq. No. 0.08;
Matches 18; Conservation 0; Mismatches 0; Indels 0; Gaps 0.
US-08-876-766-13

|||||

US-08-876-766-13

Sequence 13, Application US/08876766
Patient No. 5876978
GENERAL INFORMATION:
APPLICANT: Willey, James C.
TITLE OF INVENTION: Method for Quantitative Measurement of
TITLE OF INVENTION: Gene Expression Using Multi-Plex Competitive Reverse
TITLE OF INVENTION: Transcriptase Polymerase Chain Reaction
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Emu, Schaub, & Porcello Co.,
ADDRESS: L.P.A.
STREET: One Squarto, Suite 1980
CITY: Toledo
STATE: Ohio
ZIP: 43604
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: pc-ips/ms-dos
SOFTWARE: Paton to Release #1.9, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/188,434
FILING DATE: 28-Jan-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/043,390
FILING DATE: 06-Apr-1993
ATTORNEY/AGENT INFORMATION:
NAME: Martineau, Catherine R.
REGISTRATION NUMBER: 41,854
REFERENCE/ATTORNEY NUMBER: 34205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (419) 243-1294
TELEFAX: (419) 243-8502
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: liver
PUBLICATION INFORMATION:
AUTHORS: Tokumura, K.
AUTHORS: Nakamura, Y.
AUTHORS: Sakata, K.
AUTHORS: Fujimoto, K.
AUTHORS: Ohkubo, M.
AUTHORS: Sawada, K.
AUTHORS: Sakiyama, S.
TITLE: Enhanced expression of a
TITLE: glyceraldehyde-3-phosphate dehydrogenase gene in
TITLE: human lung cancers
JOURNAL: Cancer Res.
VOLUME: 47
PAGES: 5616-5619
DATE: SUMMER-1990
RELEVANT RESIDUES IN SEQ ID NO: 13: FROM 1 TO 24
US-08-876-766-13

Query Match 42.0% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No. 1.2
Matches 16 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 25 GGTGAGCTGAGGATT 42
|||||
DB 1 GGTGAGCTGAGGATT 18

RESULT 10
US-09-156-424-5
Sequence 5, Application US/09156424
Patent No. 5948296
FEATURE:
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF RHOA EXPRESSION
FILE REFERENCE: PUS-0012
CURRENT APPLICATION NUMBER: US/09/156 424
CURRENT FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-156-424-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No. 1.2
Matches 16 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAGCTGAGGTC 34
|||||
DB 4 GGTGAGCTGAGGTC 19

RESULT 11
US-09-213-767-5
Sequence 5, Application US/09213767
Patent No. 5948680
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
FILE REFERENCE: PUS-0024
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-213-767-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No. 1.2
Matches 16 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAGCTGAGGTC 34
|||||
DB 4 GGTGAGCTGAGGTC 19

RESULT 12
US-09-205-922-5
Sequence 5, Application US/09205922
Patent No. 5951465
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G ALPHA 1 EXPRESSION

FILE REFERENCE: PUS-0020
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-205-922-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No. 1.2
Matches 16 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAGCTGAGGTC 34
|||||
DB 4 GGTGAGCTGAGGTC 19

RESULT 13
US-09-205-144-5
Sequence 5, Application US/99205144
Patent No. 5958771
GENERAL INFORMATION:
APPLICANT: G. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APoptosis-2 (CIP2A)
FILE REFERENCE: PUS-0021
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-205-144-5

Query Match 38.1% Score 16 DB 2 Length 19
Best Local Similarity 100.0% Pred No. 1.2
Matches 16 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAGCTGAGGTC 34
|||||
DB 4 GGTGAGCTGAGGTC 19

RESULT 14
US-09-205-204-5
Sequence 5, Application US/09205204
Patent No. 5958772
GENERAL INFORMATION:
APPLICANT: G. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APoptosis-2 (CIP2A)
FILE REFERENCE: PUS-0020
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-205-204-5

Query Match 38.1% Score 16 DB 2 Length 19

Best Local Similarity: 100.0%; Prod. No. 1.2;
Matches: 16; conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAATTCGGAGTC 44
|||||
DB 4 GGTGAAATTCGGAGTC 19

RESULT 15

US-09-212-771-5
Sequence 5, Application US/09/212771
Feature No. 698873
GENERAL INFORMATION:
APPLICANT: HOOT P. MONT
TITLE OF INVENTION: ANTIGENIC REGULATION OF AKT-1 EXPRESSION
FILE REFERENCE: KIS-0044
CURRENT APPLICATION NUMBER: US/09/212771
CURRENT FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 47
SEQ ID No. 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-212-771-5

Query Match: 68.1%; Score 16; DB 2; Length 19;
Best Local Similarity: 100.0%; Prod. No. 1.2;
Matches: 16; conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAATTCGGAGTC 44
|||||
DB 4 GGTGAAATTCGGAGTC 19

Search completed: April 18, 2003, 05:10:01
Job Time: 10:09 secs

GenSoft Version 5.0.1_p5_1573
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OM nucleic acid nucleic acid search, using sw model

Run no. April 17, 2003, 20.41.01, 30 min. time 1755 seconds (without alignments)

Title: US-09-701-394-1

Sequence: 1 accgatggttgagatcctccacgaagtcaaacggaattt 42

Scoring table:

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Searched, 633749 pages, 302286378 instances

Word size :

Total number of hits satisfying chosen parameters:

Maximum DH seq length: 50

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*

Database : Published_Applications_NA:*

- 1: `new2 = new Product(1, "Apple", 2007, "NEW", COMB, 1);`
- 2: `new2 = new Product(2, "Peach", 2007, "NEW", PUR, 3);`
- 3: `new2 = new Product(3, "Apple", 2007, "NEW", PUR, 3);`
- 4: `new2 = new Product(4, "Apple", 2007, "NEW", PUR, 3);`
- 5: `new2 = new Product(5, "Apple", 2007, "NEW", PUR, 3);`
- 6: `new2 = new Product(6, "Apple", 2007, "NEW", PUR, 3);`
- 7: `new2 = new Product(7, "Peach", 2007, "NEW", PUR, 3);`
- 8: `new2 = new Product(8, "Peach", 2007, "NEW", PUR, 3);`
- 9: `new2 = new Product(9, "Peach", 2007, "NEW", PUR, 3);`
- 10: `new2 = new Product(1, "Peach", 2007, "NEW", PUR, 3);`
- 11: `new2 = new Product(1, "Peach", 2007, "NEW", PUR, 3);`
- 12: `new2 = new Product(1, "Peach", 2007, "NEW", PUR, 3);`
- 13: `new2 = new Product(1, "Peach", 2007, "NEW", PUR, 3);`
- 14: `new2 = new Product(1, "Peach", 2007, "NEW", PUR, 3);`

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result	Query	Score	Length	DB	ID	Description
C	1	57.1	28	9	US-09-09-45-A-0-1	Sequence 39, App
C	2	57.1	28	9	US-09-06-780A-00	Sequence 39, App
C	3	57.1	28	9	US-09-99-331-1	Sequence 41, App
C	4	57.1	28	9	US-09-95-556A-28	Sequence 42, App
C	5	57.1	28	9	US-09-96-48-B-25	Sequence 42, App
C	6	57.1	28	9	US-09-99-48-B-06	Sequence 42, App
C	7	57.1	28	9	US-10-101-921-37	Sequence 39, App
C	8	57.1	28	10	US-09-778-196-32	Sequence 39, App
C	9	57.1	28	10	US-09-052-604-1	Sequence 1, App
C	10	57.1	28	10	US-09-816-434-11	Sequence 1, App
C	11	57.1	28	10	US-09-932-600-1	Sequence 1, App
C	12	57.1	28	10	US-09-918-780-39	Sequence 1, App
C	13	47.6	20	10	US-09-777-732-1	Sequence 1, App
C	14	50	18	10	US-09-894-700-00	Sequence 1, App
C	15	45.5	25	10	US-09-894-713-14	Sequence 1, App
C	16	42.9	28	9	US-09-771-322-14	Sequence 41, App
C	17	38.1	19	9	US-09-901-812-15	Sequence 10, App
C	18	38.1	19	9	US-09-824-16-1	Sequence 10, App
C	19	38.1	19	9	US-09-824-322B-46	Sequence 46, App

ALLEGMENTS

20	15	42.1	19	9	US-10-233-499-50	Sequence 20, Appl
21	15	42.1	19	9	US-10-233-499-50	Sequence 20, Appl
22	15	42.1	19	9	US-09-828-864-7	Sequence 7, Appl
23	16	38.1	19	9	US-09-865-866-7	Sequence 7, Appl
24	16	38.1	19	9	US-10-156-610-5	Sequence 5, Appl
25	15	39.1	19	9	US-10-181-603-7	Sequence 7, Appl
26	16	38.1	19	9	US-09-865-993-7	Sequence 7, Appl
27	16	38.1	19	9	US-09-780-782-95	Sequence 25, Appl
28	16	38.1	19	10	US-09-067-6388-8	Sequence 89, Appl
29	15	38.1	19	10	US-09-773-794A-7	Sequence 7, Appl
30	16	38.1	19	10	US-09-854-883-7	Sequence 7, Appl
31	16	38.1	19	10	US-09-878-882-5	Sequence 5, Appl
32	15	38.1	19	10	US-09-731-5578-7	Sequence 7, Appl
33	16	38.1	19	10	US-09-918-856A-7	Sequence 7, Appl
34	16	38.1	19	10	US-09-780-1742-7	Sequence 7, Appl
35	16	38.1	19	10	US-09-791-743-7	Sequence 7, Appl
36	16	38.1	19	10	US-09-791-406-7	Sequence 7, Appl
37	15	38.1	19	10	US-09-791-942-7	Sequence 7, Appl
38	15	38.1	27	9	US-10-222-180-7	Sequence 21, Appl
39	15	35.7	18	10	US-09-956-636A-7	Sequence 7, Appl
40	15	35.7	18	10	US-09-956-636A-11	Sequence 11, Appl
41	15	35.7	24	9	US-09-829-4356A-7	Sequence 24, Appl
42	15	35.7	24	9	US-09-745-008-10	Sequence 10, Appl
43	14	33.3	22	10	US-09-804-386-1	Sequence 1, Appl
44	13	31.0	22	9	US-10-002-971-19	Sequence 49, Appl
45	13	31.0	22	12	US-10-011-279-19	Sequence 1, Appl

RESUIT 11

2010000496700
201000039. April 1994 110 2509966459P

GENERAL INFORMATION

APPLICANT: MINIER, G.

ASSISTANT. NATIONAL BUREAU OF
INVESTIGATION. P. P.

APPLICANT: PAPER, L.

FIELD OF INVENTION. A NEW METHOD OF TREATING

1111 EFFEFFNF - 10039NP
CONFIDENTIALITY NOTICE

CURRENT FILING DATE: 2001-09-26
FBI AND FBI/DOJ NUMBER: 66035 832

PRIOR FILING DATE: 2000 09 27

PRIOR FILING DATE: 2001-01-16
PRIORITY DATE: 2001-01-16
PRIORITY NUMBER: 60/300

PRIOR FILING DATE: 2001-07-13

PRICE ALL IN PATF. 2001-08-17
NUMBER OF SEQ IN NOS. 60

SOFTWARE: Patent In Vor 2.1
 2017-10-29

LENGTH: 28
TYPE: 09A

CONTINUED: All of the following
 EVAPTYPE:

THE INSTITUTE FOR THE STUDY OF THE HISTORY OF THE UNITED STATES

115. 02. 96 (450A 34

Query Method	Top 10
Fast Local Similarity	100.0%

Matches	24	conservative	10
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PRIOR APPLICATION NUMBER: 60/415,412
 PRIOR FILING DATE: 2001-04-26
 NUMBER OF SEQ ID NOS: 91
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 26
 LENGTH: 28
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-966-422B 26

Query Match: 57.1%; Score: 24; DB: 9; Length: 28;
 Best Local Similarity: 100.0%; Pred. No. 5,76-05;
 Matches: 24; Conservativ: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAGGTGGAGTCAAGGATT 42
 DB 26 GGTGAAGGTGGAGTCAAGGATT 3

RESULT 6
 US-09-992-238-02, 2
 Sequence 62, Artificially synthesized primer sequence
 Publication No. US2003064444A1
 GENERAL INFORMATION:

APPLICANT: BATTAGLINO, PETER
 APPLICANT: FEDER, JOHN N
 APPLICANT: MINTER, GABE
 APPLICANT: NELSON, THOMAS C
 APPLICANT: RAMANATHAN, CHANDRA S
 APPLICANT: WESTPHAL, RYAN
 APPLICANT: CACACE, ANGELA
 APPLICANT: BARBER, LAUREN
 APPLICANT: HARKIN, DONALD R
 APPLICANT: KORNACKER, MICHAEL G
 TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HEPHEMTR, FILE REFERENCE: 06047NP
 CURRENT APPLICATION NUMBER: US-09-992-238
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/417192
 PRIOR FILING DATE: 2001-09-04
 PRIOR APPLICATION NUMBER: 60/408-85
 PRIOR FILING DATE: 2001-07-27
 PRIOR APPLICATION NUMBER: 60/368581
 PRIOR FILING DATE: 2001-02-14
 PRIOR APPLICATION NUMBER: 60/248285
 PRIOR FILING DATE: 2000-11-14
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 62
 LENGTH: 28
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: CATER FVT
 OTHER INFORMATION: Tagged(F) Ende
 US-09-992-238-02

Query Match: 57.1%; Score: 21; DB: 9; Length: 28;
 Best Local Similarity: 100.0%; Pred. No. 5,76-05;
 Matches: 21; Conservativ: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 19 GGTGAAGGTGGAGTCAAGGATT 42
 DB 26 GGTGAAGGTGGAGTCAAGGATT 3

RESULT 7
 US-10-101-921-37
 Sequence 37, Application US/1010921
 Publication No. US2003064444A1
 GENERAL INFORMATION:
 APPLICANT: Nezu, Jun-ichi

APPLICANT: Ose, Asuka
 APPLICANT: Tsujii, Akira
 TITLE OF INVENTION: JPANPOPEPPE GENE OAP-B, C, D, AND E
 FILE REFERENCE: 06501-1040S1
 CURRENT APPLICATION NUMBER: US/1010921
 CURRENT FILING DATE: 2002-06-28
 PRIOR APPLICATION NUMBER: PCT/JP00/06416
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: JP 11/267835
 PRIOR FILING DATE: 1999-09-21
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 37
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Artificially synthesized primer sequence
 US-10-101-921-37

Query Match: 57.1%; Score: 22; DB: 9; Length: 26;
 Best Local Similarity: 100.0%; Pred. No. 0,000-07;
 Matches: 22; Conservativ: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 21 TGAAGGTGGAGTCAAGGATT 42
 DB 1 TGAAGGTGGAGTCAAGGATT 22

RESULT 8
 US-09-738-396-39
 Sequence 39, Application US/09738396
 Patent No. US2003029013A1
 GENERAL INFORMATION:
 APPLICANT: Reed, John C.
 APPLICANT: Sedzik, Adam
 TITLE OF INVENTION: BCL-2 Polypeptides, Encoding Nucleic Acids and Methods
 FILE REFERENCE: of Use
 CURRENT APPLICATION NUMBER: US-09-738-396
 CURRENT FILING DATE: 2000-12-14
 PRIOR APPLICATION NUMBER: US 09/461,641
 PRIOR FILING DATE: 1998-12-14
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 39
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 OTHER INFORMATION: primer
 US-09-738-396-39

Query Match: 52.4%; Score: 22; DB: 10; Length: 26;
 Best Local Similarity: 100.0%; Pred. No. 0,000-07;
 Matches: 22; Conservativ: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 21 TGAAGGTGGAGTCAAGGATT 42
 DB 1 TGAAGGTGGAGTCAAGGATT 22

RESULT 9
 US-09-952-604-1
 Sequence 1, Application US/09952604
 Patent No. US20020137680A1
 GENERAL INFORMATION:
 APPLICANT: Ahmed, Asif Syed
 TITLE OF INVENTION: Methods of Delaying the Onset of Labor
 FILE REFERENCE: of Use
 CURRENT APPLICATION NUMBER: US/09/952,604
 CURRENT FILING DATE: 2002-02-25

NUMBER OF SEQ ID NOS: 5
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:vascular
 OTHER INFORMATION: endothelial growth factor antisense (3') primer
 US-09-952,664-1

Query Match 52.4%; Score 22; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

21 TGAAGTCGAGTCACCGATT 42
 1 TGAAGTCGAGTCACCGATT 22

RESULT 10
 US-09-816,248-44
 Sequence 44, Application US/09/816,248
 Patent No. US2002018709A1
 GENERAL INFORMATION:
 APPLICANT: BAUMANN, PETER
 APPLICANT: CROCH, THOMAS R.
 TITLE OF INVENTION: PROTECTION OF TELOMERASE-1 (POT-1) PROTEIN AND ENCODING
 FILE REFERENCE: 08/941/0201
 CURRENT FILING DATE: 2001-03-26
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 44
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Primer
 US-09-816,248-44

Query Match 52.4%; Score 22; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

21 TGAAGTCGAGTCACCGATT 42
 1 TGAAGTCGAGTCACCGATT 22

RESULT 11
 US-09-992,860-1
 Sequence 1, Application US/09/992,860
 Patent No. US2002014472A1
 GENERAL INFORMATION:
 APPLICANT: Chen, Kuang Yu
 APPLICANT: Ho, Chi Tang
 APPLICANT: Rosen, Robert E.
 APPLICANT: Ghali, Goshka
 TITLE OF INVENTION: Block Tag Extract for Prevention of Disease
 FILE REFERENCE: 80-0173
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/248,942
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-912,860-1

Query Match 52.4%; Score 22; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

21 TGAAGTCGAGTCACCGATT 42
 1 TGAAGTCGAGTCACCGATT 22

RESULT 12
 US-09-918,702-38
 Sequence 38, Application US/09/918,702
 Patent No. US2002014667B1
 GENERAL INFORMATION:
 APPLICANT: Benvenisty, Nissim
 TITLE OF INVENTION: Directed Differentiation of Embryonic Stem
 FILE REFERENCE: 1822/113
 CURRENT FILING DATE: 2001-07-31
 NUMBER OF SEQ ID NOS: 74
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 38
 LENGTH: 26
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 CITE: 10-EMBO J. 14: 4402-4410
 OTHER INFORMATION: dehydrogenase
 US-09-918,702-38

Query Match 52.4%; Score 22; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00087;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

21 TGAAGTCGAGTCACCGATT 42
 1 TGAAGTCGAGTCACCGATT 22

RESULT 13
 US-09-777,742-1
 Sequence 1, Application US/09/777,742
 Patent No. US2002014235A1
 GENERAL INFORMATION:
 APPLICANT: Avinur, Yitzhak
 APPLICANT: Ma, Nall
 APPLICANT: Strom, Terry
 APPLICANT: Soares, Miguel C.
 APPLICANT: Ferrari, Christiano
 APPLICANT: Meikhem, Subbarayan
 TITLE OF INVENTION: MEASUREMENT OF PROTECTIVE GATES IN ANTICRAFT REDUCTION
 FILE REFERENCE: 01/948-059001
 CURRENT FILING DATE: 2001-02-06
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetically generated primer
 US-09-777,742-1

Query Match 47.6%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0181;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

19 GTTGAAGTCGAGTCACCGATT 48

Db 1 GGTGAAGGTGGAGTCAACG 20

RESULT 14

US-09-899-569A-36
Sequence 36, Application US/09899569A

Patent No. US20020142003A1

GENERAL INFORMATION:

APPLICANT: No. US20020142003Albert Schweitzer

APPLICANT: Marwa Scherl Mostager

APPLICANT: Wolfgang Sommergruber

APPLICANT: Roger Abseher

TITLE OF INVENTION: Tumorssoziales Antigen (B345)

FILE REFERENCE: 0652, 2280001

CURRENT FILING DATE: 2001-07-06

PRIOR APPLICATION NUMBER: DE 100 33 080 0

PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: DE 101 19 294 0

PRIOR FILING DATE: 2001-04-19

PRIOR APPLICATION NUMBER: US 60/243,158

PRIOR FILING DATE: 2000-10-25

PRIOR APPLICATION NUMBER: US 60/297,747

PRIOR FILING DATE: 2001-06-14

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 36

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial sequence

OTHER INFORMATION: Description of the artificial sequence: Primer

US-09-899-569A-36

Query Match

Best Local Similarity: 47.6%; Score 20; DB 10; Length 22;

Match: 20; Conserved: 0; Mismatches: 0; Trunc: 0; Gaps: 0;

QY 19 GGTGAAGGTGGAGTCAACG 38

Db 1 GGTGAAGGTGGAGTCAACG 22

RESULT 15

US-09-897-412-4
Sequence 4, Application US/09897412

Patent No. US20020142956A1

GENERAL INFORMATION:

APPLICANT: Davis, Richard J

APPLICANT: Page, Keith J

TITLE OF INVENTION: Use of Secretin Receptor Ligands in Treatment of Cystic

TITLE OF INVENTION: Fibrosis (CF) and Chronic Obstructive Pulmonary Disease

FILE REFERENCE: 620-148

CURRENT APPLICATION NUMBER: US/20/897,412

CURRENT FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: GB 0016441.8

PRIOR FILING DATE: 2000-07-04

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-897-412-4

Query Match

Best Local Similarity: 45.2%; Score 19; DB 10; Length 22;

Match: 19; Conserved: 0; Mismatches: 0; Trunc: 0; Gaps: 0;

QY 19 GGTGAAGGTGGAGTCAAC 37

Db 4 GGTGAAGGTGGAGTCAAC 22

Search completed: April 18, 2003, 21:45:40
Job time: 1956 secs

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1 APPLICANT: FEDER, J. N.
2 APPLICANT: MINTER, J.
3 APPLICANT: RAMANATHAN, C. S.
4 APPLICANT: HARKEN, D. R.
5 APPLICANT: CACACE, A.
6 TITLE OF INVENTION: A NOVEL HUMAN G PROTEIN COUPLED RECEPTOR, EXPRESSED
7 FILE REFERENCE: D0045NP
8 CURRENT FILING DATE: 2001-09-26
9 PRIOR APPLICATION NUMBER: 60/261,776
10 PRIOR FILING DATE: 2001-08-08
11 PRIOR APPLICATION NUMBER: 60/261,776
12 PRIOR FILING DATE: 2001-01-16
13 PRIOR APPLICATION NUMBER: 60/261,776
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: 60/261,776
16 SOFTWARE: Patent In Ver. 2.1
17 SEQ ID NO 35
18 LENGTH: 28
19 TYPE: DNA
20 ORGANISM: Artificial Sequence
21 FEATURE:
22 OTHER INFORMATION: Description of Artificial Sequence: GAPDH-PVIC
23 US-09-964-923A-39

```

```

Query Match 57.1% Score 24 DB 36 Length 28
Best Local Similarity 100.0% Prod No 0.0012
Matches 24 Conserved 0 Mismatches 0 Indels 0 Gaps 0
QY 19 GGTGAAGTGGAGTCACAGGATT 42
DB 26 GGTGAAGTGGAGTCACAGGATT 3

```

```

RESULT 5
US-09-965-536A-28/C
1 Sequence 29, Application US/09066459A
2 GENERAL INFORMATION:
3 APPLICANT: FEDER, J. N.
4 APPLICANT: MINTER, J.
5 APPLICANT: RAMANATHAN, C. S.
6 APPLICANT: HARKEN, D. R.
7 APPLICANT: CACACE, A.
8 TITLE OF INVENTION: A NOVEL HUMAN G PROTEIN COUPLED RECEPTOR, EXPRESSED
9 FILE REFERENCE: D0045NP
10 CURRENT FILING DATE: 2001-09-26
11 PRIOR APPLICATION NUMBER: 60/261,776
12 PRIOR FILING DATE: 2001-08-08
13 PRIOR APPLICATION NUMBER: 60/261,776
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: 60/261,776
16 PRIOR FILING DATE: 2001-01-16
17 PRIOR APPLICATION NUMBER: 60/261,776
18 SOFTWARE: Patent In Ver. 2.1
19 SEQ ID NO 28
20 LENGTH: 28
21 TYPE: DNA
22 ORGANISM: Artificial Sequence
23 FEATURE:
24 OTHER INFORMATION: Description of Artificial Sequence: GAPDH-PVIC
25 US-09-965-536A-28

```

```

Query Match 57.1% Score 24 DB 36 Length 28
Best Local Similarity 100.0% Prod No 0.0012
Matches 24 Conserved 0 Mismatches 0 Indels 0 Gaps 0
QY 19 GGTGAAGTGGAGTCACAGGATT 42

```

```

DB 26 GGTGAAGTGGAGTCACAGGATT 3
RESULT 6
US-09-966-422B-36/C
1 Sequence 29, Application US/09066422B
2 GENERAL INFORMATION:
3 APPLICANT: FEDER, J. N.
4 APPLICANT: MINTER, J.
5 APPLICANT: RAMANATHAN, C. S.
6 APPLICANT: HARKEN, D. R.
7 APPLICANT: CACACE, A.
8 TITLE OF INVENTION: A NOVEL HUMAN G PROTEIN COUPLED RECEPTOR, EXPRESSED
9 FILE REFERENCE: D0045NP
10 CURRENT FILING DATE: 2001-09-26
11 PRIOR APPLICATION NUMBER: 60/261,776
12 PRIOR FILING DATE: 2001-08-08
13 PRIOR APPLICATION NUMBER: 60/261,776
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: 60/261,776
16 SOFTWARE: Patent In Ver. 2.1
17 SEQ ID NO 26
18 LENGTH: 28
19 TYPE: DNA
20 ORGANISM: Homo sapiens
21 US-09-966-422B-26

```

```

Query Match 57.1% Score 24 DB 36 Length 28
Best Local Similarity 100.0% Prod No 0.0012
Matches 24 Conserved 0 Mismatches 0 Indels 0 Gaps 0
QY 19 GGTGAAGTGGAGTCACAGGATT 42
DB 26 GGTGAAGTGGAGTCACAGGATT 3

```

```

RESULT 7
US-09-966-459A-29/C
1 Sequence 29, Application US/09066459A
2 GENERAL INFORMATION:
3 APPLICANT: FEDER, J. N.
4 APPLICANT: MINTER, J.
5 APPLICANT: RAMANATHAN, C. S.
6 APPLICANT: HARKEN, D. R.
7 APPLICANT: CACACE, A.
8 TITLE OF INVENTION: A NOVEL HUMAN G PROTEIN COUPLED RECEPTOR, EXPRESSED
9 FILE REFERENCE: D0039NP
10 CURRENT FILING DATE: 2001-09-26
11 PRIOR APPLICATION NUMBER: 60/261,776
12 PRIOR FILING DATE: 2001-08-08
13 PRIOR APPLICATION NUMBER: 60/261,776
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: 60/261,776
16 PRIOR FILING DATE: 2001-01-16
17 PRIOR APPLICATION NUMBER: 60/261,776
18 SOFTWARE: Patent In Ver. 2.1
19 SEQ ID NO 29
20 LENGTH: 28
21 TYPE: DNA
22 ORGANISM: Artificial Sequence
23 FEATURE:
24 OTHER INFORMATION: Description of Artificial Sequence: GAPDH-PVIC
25 US-09-966-459A-29

```

```

Query Match 57.1% Score 24 DB 36 Length 28

```

Best Local Similarity: 100.0%, Prod. No. 0.00121
Matches: 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGTGGAGTCAAGCAAT 42
|||||
DB 26 GGTGAAGTGGAGTCAAGCAAT 4

RESULT 9

US-09-992-782A-4476

Sequence 43, Application US/09996782A

GENERAL INFORMATION:

APPLICANT: Battaglini, P.

APPLICANT: Feder, J. N.

APPLICANT: Mintoff, G.

APPLICANT: Ramanathan, C. S.

APPLICANT: Westphal, R.

APPLICANT: Harker, D. R.

APPLICANT: Farago, A.

APPLICANT: Barber, L.

APPLICANT: Kottacker, M. J.

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRM7,

FILE REFERENCE: 10044ND

CURRENT APPLICATION NUMBER: US/09/966,782A

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/245,731

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/246,590

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/217,121

PRIOR FILING DATE: 2001-08-28

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PatGen Ver. 2.1

SEQ ID NO: 42

LENGTH: 28

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CAPRI FV1

US-09-966-782A-43

Query Match: 57.1%, Score 24, FR 46, Length 28,

Best Local Similarity: 100.0%, Prod. No. 0.00121

Matches: 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGTGGAGTCAAGCAAT 42
|||||

DB 26 GGTGAAGTGGAGTCAAGCAAT 4

RESULT 9

US-09-992-782A-4476

Sequence 42, Application US/09996782A

GENERAL INFORMATION:

APPLICANT: Battaglini, PETER

APPLICANT: Feder, JOHN N

APPLICANT: MINTIER, GABE

APPLICANT: NELSON, THOMAS C

APPLICANT: RAMANATHAN, CHANDRA S

APPLICANT: WESTPHAL, RYAN

APPLICANT: FARAGO, ANGELA

APPLICANT: HARKER, LAGREN

APPLICANT: HARKER, DONALD R

APPLICANT: KOTTACKER, MICHAEL G

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRM7,

FILE REFERENCE: 10044ND

CURRENT APPLICATION NUMBER: US/09/992,782A

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/217,121

PRIOR FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/308285

PRIOR FILING DATE: 2001-07-27

PRIOR APPLICATION NUMBER: 60/268581

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/248285

PRIOR FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatGen Ver. 2.1

SEQ ID NO: 62

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CAPRI FV1

US-09-992-238-62

Query Match: 57.1%, Score 24, FR 46, Length 28,

Best Local Similarity: 100.0%, Prod. No. 0.00121

Matches: 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGTGGAGTCAAGCAAT 42
|||||

DB 26 GGTGAAGTGGAGTCAAGCAAT 4

RESULT 10

US-09-992-841-4176

Sequence 41, Application US/09992841

GENERAL INFORMATION:

APPLICANT: FEDER, JOHN N.

APPLICANT: MINTIER, GABE

APPLICANT: RAMANATHAN, CHANDRA S.

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPGRM7,

FILE REFERENCE: 10044ND

CURRENT APPLICATION NUMBER: US/09/992,841

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/261,782

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: 60/217,121

PRIOR FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatGen Ver. 2.1

SEQ ID NO: 41

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CAPRI FV1

US-09-992-341-41

Query Match: 57.1%, Score 24, FR 46, Length 28,

Best Local Similarity: 100.0%, Prod. No. 0.00121

Matches: 24 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 19 GGTGAAGTGGAGTCAAGCAAT 42
|||||

DB 26 GGTGAAGTGGAGTCAAGCAAT 4

RESULT 11

US-10-120-604-18476

Sequence 184, Application US/10120604

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: PEPTIDOMIMETIC ANALOGS OF TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS, HGPGRM7 AND HGPGRM8, AND THEIR VARIANTS THEREOF

Mon Apr 21 08:33:23 2003

us-09-701-394-1.rmpm

Page 6

Search completed: April 18, 2003, 18:44:58
Index time: 48820 secs


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1 CURRENT FILING DATE: 2002-10-11
2 PRIOR APPLICATION NUMBER: U.S. 60/328,479
3 PRIOR FILING DATE: 2001-10-11
4 NUMBER OF SEQ. ID NOS: 95
5 SOFTWARE: Patent In version 4.1
6 SEQ. ID NO: 97
7 LENGTH: 28
8 TYPE: DNA
9 ORGANISM: Homo sapiens
10-10-271-078 93

```

```

Query Match: 57.1%, Score 24; DB 97, Length 28;
Best Local Similarity: 100.0%, Prod. No. 0.00045;
Matches 24; Conserved: 0; Mismatches 0; Indels 0; Gaps 0;

```

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07 19 GGTGAAGGTGGAGTCAAGCAAT 42
10 26 GGTGAAGGTGGAGTCAAGCAAT 4

```

```

RESULT 4
US-10-423-412-29/7

```

```

1 Sequence 29, Application US/10423412
2 GENERAL INFORMATION:
3 APPLICANT: Bristol-Myers Squibb Company
4 TITLE OF INVENTION: REVEL HUMAN G PROTEIN COUPLED RECEPTOR, HEPHRMY4, AND METHODS OF
5 TITLE OF INVENTION: THEREOF
6 FILE REFERENCE: 100330A CIP
7 CURRENT APPLICATION NUMBER: US/10-423-412
8 PRIOR FILING DATE: 2002-12-18
9 PRIOR APPLICATION NUMBER: U.S. 09/964,459
10 PRIOR FILING DATE: 2001-09-26
11 PRIOR APPLICATION NUMBER: U.S. 60/245,833
12 PRIOR FILING DATE: 2000-09-27
13 PRIOR APPLICATION NUMBER: U.S. 60/261,776
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: U.S. 60/405,451
16 PRIOR FILING DATE: 2001-07-14
17 PRIOR APPLICATION NUMBER: U.S. 60/413,202
18 PRIOR FILING DATE: 2001-08-17
19 NUMBER OF SEQ. ID NOS: 69
20 SOFTWARE: Patent In version 4.1
21 SEQ. ID NO: 29
22 LENGTH: 28
23 TYPE: DNA
24 ORGANISM: Homo sapiens
25-10-423-412-29

```

```

Query Match: 57.1%, Score 24; DB 97, Length 28;
Best Local Similarity: 100.0%, Prod. No. 0.00045;
Matches 24; Conserved: 0; Mismatches 0; Indels 0; Gaps 0;
07 19 GGTGAAGGTGGAGTCAAGCAAT 42
10 26 GGTGAAGGTGGAGTCAAGCAAT 4

```

```

RESULT 4

```

```

US-10-262-272A 26/7
1 Sequence 26, Application US/10262272A
2 GENERAL INFORMATION:
3 APPLICANT: Bristol-Myers Squibb Company
4 TITLE OF INVENTION: REVEL HUMAN G PROTEIN COUPLED RECEPTOR, HEPHRMY4
5 FILE REFERENCE: 10044 CIP
6 CURRENT APPLICATION NUMBER: US/10-262-272A
7 CURRENT FILING DATE: 2002-09-27
8 PRIOR APPLICATION NUMBER: U.S. 09/966,422
9 PRIOR FILING DATE: 2001-09-26
10 PRIOR APPLICATION NUMBER: U.S. 09/966,422
11 PRIOR FILING DATE: 2001-09-26
12 NUMBER OF SEQ. ID NOS: 91
13 SOFTWARE: Patent In version 4.2
14 SEQ. ID NO: 26
15 LENGTH: 28
16 TYPE: DNA

```

```

1 ORGANISM: Homo sapiens
2 US-10-262-272A 26

```

```

Query Match: 57.1%, Score 24; DB 97, Length 28;
Best Local Similarity: 100.0%, Prod. No. 0.00045;
Matches 24; Conserved: 0; Mismatches 0; Indels 0; Gaps 0;
07 19 GGTGAAGGTGGAGTCAAGCAAT 42
10 26 GGTGAAGGTGGAGTCAAGCAAT 4

```

```

07 19 GGTGAAGGTGGAGTCAAGCAAT 42
10 26 GGTGAAGGTGGAGTCAAGCAAT 4

```

```

RESULT 5

```

```

US-10-348-119 795/76
1 Sequence 795, Application US/10348119
2 GENERAL INFORMATION:
3 APPLICANT: Bristol-Myers Squibb Company
4 TITLE OF INVENTION: IDENTIFICATION OF POLYPEPTIDES AND PEPTIDE FOR PROTECTI
5 TITLE OF INVENTION: ACTIVITY OF PEPTIDES THAT INTERACT WITH PROTEIN TYROSINE KIN
6 TITLE OF INVENTION: ASK/JNK PROTEIN TYROSINE KINASE PATHWAYS
7 FILE REFERENCE: 10185 NP
8 CURRENT APPLICATION NUMBER: US/10-348-119
9 PRIOR FILING DATE: 2003-01-17
10 PRIOR APPLICATION NUMBER: US 60/7450,061
11 PRIOR FILING DATE: 2002-01-18
12 NUMBER OF SEQ. ID NOS: 795
13 SOFTWARE: Patent In version 4.2
14 SEQ. ID NO: 795
15 LENGTH: 28
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18-10-348-119-795

```

```

Query Match: 57.1%, Score 24; DB 97, Length 28;
Best Local Similarity: 100.0%, Prod. No. 0.00045;
Matches 24; Conserved: 0; Mismatches 0; Indels 0; Gaps 0;
07 19 GGTGAAGGTGGAGTCAAGCAAT 42
10 26 GGTGAAGGTGGAGTCAAGCAAT 4

```

```

RESULT 6

```

```

US-60-446-655-42/0
1 Sequence 32, Application US/60446655
2 GENERAL INFORMATION:
3 APPLICANT: Bristol-Myers Squibb Company
4 TITLE OF INVENTION: IDENTIFICATION OF HUMAN G PROTEIN COUPLED RECEPTORS
5 FILE REFERENCE: 10286 PSP
6 CURRENT APPLICATION NUMBER: US/60-446-655
7 CURRENT FILING DATE: 2004-02-11
8 NUMBER OF SEQ. ID NOS: 112
9 SOFTWARE: Patent In version 4.2
10 SEQ. ID NO: 32
11 LENGTH: 28
12 TYPE: DNA
13 ORGANISM: Artificial
14 FEATURE:
15 OTHER INFORMATION: oligonucleotide
16-60-446-655-42

```

```

Query Match: 57.1%, Score 24; DB 11, Length 28;
Best Local Similarity: 100.0%, Prod. No. 0.00045;
Matches 24; Conserved: 0; Mismatches 0; Indels 0; Gaps 0;
07 19 GGTGAAGGTGGAGTCAAGCAAT 42
10 26 GGTGAAGGTGGAGTCAAGCAAT 4

```

```

07 19 GGTGAAGGTGGAGTCAAGCAAT 42
10 26 GGTGAAGGTGGAGTCAAGCAAT 4

```

```

RESULT 7
US-10-439-11A 1

```

```

: Sequence 1: Application PC/TUS0143931A
: GENERAL INFORMATION:
: APPLICANT: Chen, Kiang Yu
: APPLICANT: Ho, Chi-Tang
: APPLICANT: Rosen, Robert T.
: APPLICANT: Chai, Geetha
: APPLICANT: Rutgers, The State University
: TITLE OF INVENTION: Black Tea Extract for Prevention of Disease
: FILE REFERENCE: RU-0172
: CURRENT APPLICATION NUMBER: PCT/US01/43931A
: CURRENT FILING DATE: 2002-06-14
: PRIOR FILING DATE: 2002-04-02
: PRIOR FILING DATE: 2000-11-15
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 1
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
PCT-US01-43931A-1

```

```

Query Match          52.4%, Score 22: FR 1: Length 26:
Best Local Similarity 100.0%, Pred. No. 0.0063:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
UY 21 TGAAGTCGAGTCACGCGATT 42
|||||
DB 1 TGAAGTCGAGTCACGCGATT 22

```

```

RESULT 8
US-09-738-396A-39
: Sequence 39: Application US/09/48396A
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Godzik, Adam
: TITLE OF INVENTION: p1-C Polypeptides, Encoding Nucleic Acids and Methods
: FILE REFERENCE: P-1-1 4450
: CURRENT APPLICATION NUMBER: US/09/738,396A
: CURRENT FILING DATE: 2000-12-14
: PRIOR APPLICATION NUMBER: US 09/461,641
: PRIOR FILING DATE: 1999-12-14
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 39
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: primer
US-09-738-396A-39

```

```

Query Match          52.4%, Score 22: FR 7: Length 26:
Best Local Similarity 100.0%, Pred. No. 0.0063:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
UY 23 TGAAGTCGAGTCACGCGATT 42
|||||
DB 1 TGAAGTCGAGTCACGCGATT 22

```

```

RESULT 9
US-10-275-172-5
: Sequence 5: Application US/10/275172
: GENERAL INFORMATION:
: APPLICANT: Merck Patent GmbH
: TITLE OF INVENTION: New Threonine-serine kinase (HISK1)
: FILE REFERENCE: htsk1bws
: CURRENT APPLICATION NUMBER: US/10/275,172

```

```

: CURRENT FILING DATE: 2002-11-04
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 5
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: primer 3
US-10-275-172-5

```

```

Query Match          52.4%, Score 22: FR 9: Length 26:
Best Local Similarity 100.0%, Pred. No. 0.0063:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
UY 21 TGAAGTCGAGTCACGCGATT 42
|||||
DB 1 TGAAGTCGAGTCACGCGATT 22

```

```

RESULT 10
US-10-275-556-5
: Sequence 5: Application US/10/275556
: GENERAL INFORMATION:
: APPLICANT: Merck Patent GmbH
: TITLE OF INVENTION: Serine-threonine kinase 3 (Htsk-3)
: FILE REFERENCE: htsk3bws
: CURRENT APPLICATION NUMBER: US/10/275,556
: CURRENT FILING DATE: 2002-11-07
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 5
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: primer 4
US-10-275-556-5

```

```

Query Match          52.4%, Score 22: FR 9: Length 26:
Best Local Similarity 100.0%, Pred. No. 0.0063:
Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
UY 21 TGAAGTCGAGTCACGCGATT 42
|||||
DB 1 TGAAGTCGAGTCACGCGATT 22

```

```

RESULT 11
US-60-434-165-26
: Sequence 26: Application US/60/434165
: GENERAL INFORMATION:
: APPLICANT: Malzok, Martin M.
: APPLICANT: Wu, Xuemuel
: APPLICANT: Wang, Pei
: APPLICANT: Bai, Yuchen
: TITLE OF INVENTION: Contrastive targets
: FILE REFERENCE: p01425054
: CURRENT FILING DATE: 2002-12-17
: PRIOR APPLICATION NUMBER: US 60/444,864
: PRIOR FILING DATE: 2001-04-27
: PRIOR APPLICATION NUMBER: US 60/411,262
: PRIOR FILING DATE: 2002-09-17
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: Patent In version 3.1
: SEQ ID NO 26
: LENGTH: 26
: TYPE: DNA
: ORGANISM: Human
US-60-434-165-26

```

```

Query Match          52.4%, Score 22: FR 11: Length 26:

```

Best Local Similarity 100.0% Prod. No. 0.00643
Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 21 TGAAGTCGAGTCACGAGATT 42

DB 1 TGAAGTCGAGTCACGAGATT 22

RESULT 12

US 60-442-164-26

Sequence 26, Application US/60442164

GENERAL INFORMATION:

APPLICANT: Matzok, Martin M.

APPLICANT: Wu, Xiumei

APPLICANT: Wang, Juei

APPLICANT: Bai, Yuchun

TITLE OF INVENTION: Sustained Effective Targeting

FILE REFERENCE: 001925985

CURRENT APPLICATION NUMBER: 02/604439-791

PRIOR FILING DATE: 2004-01-14

PRIOR APPLICATION NUMBER: US 09/2944,864

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: US 09/44,343

PRIOR FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: US 09/441,373

PRIOR FILING DATE: 2002-09-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 4.1

SEQ ID NO 26

LENGTH: 26

TYPE: DNA

ORGANISM: Human

US 60-442-164-26

Query Match 52.4% Score 22 DB 11 Length 26

Best Local Similarity 100.0% Prod. No. 0.00643

Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 21 TGAAGTCGAGTCACGAGATT 42

DB 1 TGAAGTCGAGTCACGAGATT 22

RESULT 13

US 60-442-164-26

Sequence 26, Application US/60442164

GENERAL INFORMATION:

APPLICANT: Matzok, Martin M.

APPLICANT: Wu, Xiumei

APPLICANT: Wang, Juei

APPLICANT: Bai, Yuchun

TITLE OF INVENTION: Sustained Effective Targeting

FILE REFERENCE: 001925986

CURRENT APPLICATION NUMBER: US 09/442,194

PRIOR FILING DATE: 2003-01-24

PRIOR APPLICATION NUMBER: US 09/44,864

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: US 60/444,165

PRIOR FILING DATE: 2002-12-17

PRIOR APPLICATION NUMBER: US 60/441,252

PRIOR FILING DATE: 2002-09-17

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn version 4.1

SEQ ID NO 26

LENGTH: 26

TYPE: DNA

ORGANISM: Human

US 60-442-164-26

Query Match 52.4% Score 22 DB 11 Length 26

Best Local Similarity 100.0% Prod. No. 0.00643

Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 21 TGAAGTCGAGTCACGAGATT 42

DB 1 TGAAGTCGAGTCACGAGATT 22

RESULT 14

US-09-778-0143-1

Sequence 1, Application US/09778013

GENERAL INFORMATION:

APPLICANT: Strom, Terry B.

APPLICANT: Subhadhiran, Manikam

APPLICANT: Vasconcelos, Paulo

TITLE OF INVENTION: METHOD OF EVALUATING TRANSPLANT REJECTION

FILE REFERENCE: 01948-061001

CURRENT APPLICATION NUMBER: US 09/778,013

PRIOR FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US 09/778,013

PRIOR FILING DATE: 2003-01-24

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: US 09/240,735

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